

## SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> Process for the production of polyunsaturated  
fatty acids in plants

<130> 2002/271

<140> 2002\_271

<141> 2002-04-26

<160> 64

<170> PatentIn Vers. 2.0

<210> 1

<211> 1687

<212> DNA

<213> Borago officinalis

<220>

<221> CDS

<222> (42)..(1388)

<223>  $\Delta 6$ -desaturase

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aag aaa tac att acc tca gat gaa ctc aag aac cac gat aaa ccc gga 104

Lys Lys Tyr Ile Thr Ser Asp Glu Leu Lys Asn His Asp Lys Pro Gly

10

15

20

gat cta tgg atc tcg att caa ggg aaa gcc tat gat gtt tcg gat tgg 152

Asp Leu Trp Ile Ser Ile Gln Gly Lys Ala Tyr Asp Val Ser Asp Trp

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gtg	aaa	gac	cat	cca	ggt	ggc	agc	ttt	ccc	ttg	aag	agt	ctt	gct	ggt	200
Val	Lys	Asp	His	Pro	Gly	Gly	Ser	Phe	Pro	Leu	Lys	Ser	Leu	Ala	Gly	
	40						45						50			
caa	gag	gta	act	gat	gca	ttt	gtt	gca	ttc	cat	cct	gcc	tct	aca	tgg	248
Gln	Glu	Val	Thr	Asp	Ala	Phe	Val	Ala	Phe	His	Pro	Ala	Ser	Thr	Trp	
	55						60						65			
aag	aat	ctt	gat	aag	ttt	ttc	act	ggg	tat	tat	ctt	aaa	gat	tac	tct	296
Lys	Asn	Leu	Asp	Lys	Phe	Phe	Thr	Gly	Tyr	Tyr	Leu	Lys	Asp	Tyr	Ser	
	70					75					80				85	
gtt	tct	gag	gtt	tct	aaa	gat	tat	agg	aag	ctt	gtg	ttt	gag	ttt	tct	344
Val	Ser	Glu	Val	Ser	Lys	Asp	Tyr	Arg	Lys	Leu	Val	Phe	Glu	Phe	Ser	
				90					95					100		
aaa	atg	ggt	ttg	tat	gac	aaa	aaa	ggt	cat	att	atg	ttt	gca	act	ttg	392
Lys	Met	Gly	Leu	Tyr	Asp	Lys	Lys	Gly	His	Ile	Met	Phe	Ala	Thr	Leu	
			105						110					115		
tgc	ttt	ata	gca	atg	ctg	ttt	gct	atg	agt	gtt	tat	ggg	gtt	ttg	ttt	440
Cys	Phe	Ile	Ala	Met	Leu	Phe	Ala	Met	Ser	Val	Tyr	Gly	Val	Leu	Phe	
		120						125					130			
tgt	gag	ggt	gtt	ttg	gta	cat	ttg	ttt	tct	ggg	tgt	ttg	atg	ggg	ttt	488
Cys	Glu	Gly	Val	Leu	Val	His	Leu	Phe	Ser	Gly	Cys	Leu	Met	Gly	Phe	
	135						140					145				
ctt	tgg	att	cag	agt	ggt	tgg	att	gga	cat	gat	gct	ggg	cat	tat	atg	536
Leu	Trp	Ile	Gln	Ser	Gly	Trp	Ile	Gly	His	Asp	Ala	Gly	His	Tyr	Met	
	150					155					160				165	
gta	gtg	tct	gat	tca	agg	ctt	aat	aag	ttt	atg	ggt	att	ttt	gct	gca	584
Val	Val	Ser	Asp	Ser	Arg	Leu	Asn	Lys	Phe	Met	Gly	Ile	Phe	Ala	Ala	
					170					175				180		
aat	tgt	ctt	tca	gga	ata	agt	att	ggt	tgg	tgg	aaa	tgg	aac	cat	aat	632
Asn	Cys	Leu	Ser	Gly	Ile	Ser	Ile	Gly	Trp	Trp	Lys	Trp	Asn	His	Asn	
		185							190					195		

gca cat cac att gcc tgt aat agc ctt gaa tat gac cct gat tta caa 680  
 Ala His His Ile Ala Cys Asn Ser Leu Glu Tyr Asp Pro Asp Leu Gln  
 200 205 210

tat ata cca ttc ctt gtt gtg tct tcc aag ttt ttt ggt tca ctc acc 728  
 Tyr Ile Pro Phe Leu Val Val Ser Ser Lys Phe Phe Gly Ser Leu Thr  
 215 220 225

tct cat ttc tat gag aaa agg ttg act ttt gac tct tta tca aga ttc 776  
 Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp Ser Leu Ser Arg Phe  
 230 235 240 245

ttt gta agt tat caa cat tgg aca ttt tac cct att atg tgt gct gct 824  
 Phe Val Ser Tyr Gln His Trp Thr Phe Tyr Pro Ile Met Cys Ala Ala  
 250 255 260

agg ctc aat atg tat gta caa tct ctc ata atg ttg ttg acc aag aga 872  
 Arg Leu Asn Met Tyr Val Gln Ser Leu Ile Met Leu Leu Thr Lys Arg  
 265 270 275

aat gtg tcc tat cga gct cat gaa ctc ttg gga tgc cta gtg ttc tcg 920  
 Asn Val Ser Tyr Arg Ala His Glu Leu Leu Gly Cys Leu Val Phe Ser  
 280 285 290

att tgg tac ccg ttg ctt gtt tct tgt ttg cct aat tgg ggt gaa aga 968  
 Ile Trp Tyr Pro Leu Leu Val Ser Cys Leu Pro Asn Trp Gly Glu Arg  
 295 300 305

att atg ttt gtt att gca agt ttg tca gtg act gga atg caa caa gtt 1016  
 Ile Met Phe Val Ile Ala Ser Leu Ser Val Thr Gly Met Gln Gln Val  
 310 315 320 325

cag ttc tcc ttg aac cac ttc tct tca agt gtt tat gtt gga aag cct 1064  
 Gln Phe Ser Leu Asn His Phe Ser Ser Ser Val Tyr Val Gly Lys Pro  
 330 335 340

aaa ggg aat aat tgg ttt gag aaa caa acg gat ggg aca ctt gac att 1112  
 Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp Gly Thr Leu Asp Ile  
 345 350 355

tct tgt cct cct tgg atg gat tgg ttt cat ggt gga ttg caa ttc caa 1160  
 Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly Gly Leu Gln Phe Gln  
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att gag cat cat ttg ttt ccc aag atg cct aga tgc aac ctt agg aaa 1208  
 Ile Glu His His Leu Phe Pro Lys Met Pro Arg Cys Asn Leu Arg Lys  
           375                          380                          385

atc tcg ccc tac gtg atc gag tta tgc aag aaa cat aat ttg cct tac 1256  
 Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys His Asn Leu Pro Tyr  
           390                          395                          400                          405

aat tat gca tct ttc tcc aag gcc aat gaa atg aca ctc aga aca ttg 1304  
 Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met Thr Leu Arg Thr Leu  
                           410                          415                          420

agg aac aca gca ttg cag gct agg gat ata acc aag ccg ctc ccg aag 1352  
 Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr Lys Pro Leu Pro Lys  
                           425                          430                          435

aat ttg gta tgg gaa gct ctt cac act cat ggt taa aattaccctt 1398  
 Asn Leu Val Trp Glu Ala Leu His Thr His Gly  
           440                          445

agttcatgta ataatttgag attatgtatc tcctatgttt gtgtcttgtc ttggttctac 1458

ttgttgaggat cattgcaact tgtcttttat ggtttattag atgtttttta atatatttta 1518

gaggttttgc tttcatctcc attattgatg aataaggagt tgcattattgt caattgttgt 1578

gctcaatatc tgatattttg gaatgtactt tgtaccactg tgttttcagt tgaagctcat 1638

gtgtacttct atagactttg tttaaatggg tatgaaaaaa aaaaaaaaaa 1687

<210> 2

<211> 448

<212> PRT

<213> Borago officinalis



&lt;400&gt; 2

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Asp Val Ser Asp Trp Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu  
 35 40 45

Lys Ser Leu Ala Gly Gln Glu Val Thr Asp Ala Phe Val Ala Phe His  
 50 55 60

Pro Ala Ser Thr Trp Lys Asn Leu Asp Lys Phe Phe Thr Gly Tyr Tyr  
 65 70 75 80

Leu Lys Asp Tyr Ser Val Ser Glu Val Ser Lys Asp Tyr Arg Lys Leu  
 85 90 95

Val Phe Glu Phe Ser Lys Met Gly Leu Tyr Asp Lys Lys Gly His Ile  
 100 105 110

Met Phe Ala Thr Leu Cys Phe Ile Ala Met Leu Phe Ala Met Ser Val  
 115 120 125

Tyr Gly Val Leu Phe Cys Glu Gly Val Leu Val His Leu Phe Ser Gly  
 130 135 140

Cys Leu Met Gly Phe Leu Trp Ile Gln Ser Gly Trp Ile Gly His Asp  
 145 150 155 160

Ala Gly His Tyr Met Val Val Ser Asp Ser Arg Leu Asn Lys Phe Met  
 165 170 175

Gly Ile Phe Ala Ala Asn Cys Leu Ser Gly Ile Ser Ile Gly Trp Trp  
 180 185 190

Lys Trp Asn His Asn Ala His His Ile Ala Cys Asn Ser Leu Glu Tyr  
 195 200 205

Asp Pro Asp Leu Gln Tyr Ile Pro Phe Leu Val Val Ser Ser Lys Phe  
 210 215 220

Phe Gly Ser Leu Thr Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp  
 225 230 235 240

Ser Leu Ser Arg Phe Phe Val Ser Tyr Gln His Trp Thr Phe Tyr Pro  
 245 250 255

Ile Met Cys Ala Ala Arg Leu Asn Met Tyr Val Gln Ser Leu Ile Met  
 260 265 270

Leu Leu Thr Lys Arg Asn Val Ser Tyr Arg Ala His Glu Leu Leu Gly  
 275 280 285

Cys Leu Val Phe Ser Ile Trp Tyr Pro Leu Leu Val Ser Cys Leu Pro  
 290 295 300

Asn Trp Gly Glu Arg Ile Met Phe Val Ile Ala Ser Leu Ser Val Thr  
 305 310 315 320

Gly Met Gln Gln Val Gln Phe Ser Leu Asn His Phe Ser Ser Ser Val  
 325 330 335

Tyr Val Gly Lys Pro Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp  
 340 345 350

Gly Thr Leu Asp Ile Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly  
 355 360 365

Gly Leu Gln Phe Gln Ile Glu His His Leu Phe Pro Lys Met Pro Arg  
 370 375 380

Cys Asn Leu Arg Lys Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys  
 385 390 395 400

His Asn Leu Pro Tyr Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met  
 405 410 415

Thr Leu Arg Thr Leu Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr

420

425

430

Lys Pro Leu Pro Lys Asn Leu Val Trp Glu Ala Leu His Thr His Gly

435

440

445

&lt;210&gt; 3

&lt;211&gt; 1192

&lt;212&gt; DNA

&lt;213&gt; Physcomitrella patens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (58)..(930)

&lt;223&gt; Δ6-elongase

&lt;400&gt; 3

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atg gag gtc gtg gag aga ttc tac ggt gag ttg gat ggg aag gtc tcg 105

Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser

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5

10

15

cag ggc gtg aat gca ttg ctg ggt agt ttt ggg gtg gag ttg acg gat 153

Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp

20

25

30

acg ccc act acc aaa ggc ttg ccc ctc gtt gac agt ccc aca ccc atc 201

Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile

35

40

45

gtc ctc ggt gtt tct gta tac ttg act att gtc att gga ggg ctt ttg 249

Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu

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55

60

tgg ata aag gcc agg gat ctg aaa ccg cgc gcc tcg gag cca ttt ttg 297

Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu

65

70

75

80

ctc caa gct ttg gtg ctt gtg cac aac ctg ttc tgt ttt gcg ctc agt 345

Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser	
85 90 95	
ctg tat atg tgc gtg ggc atc gct tat cag gct att acc tgg cgg tac	393
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr	
100 105 110	
tct ctc tgg ggc aat gca tac aat cct aaa cat aaa gag atg gcg att	441
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile	
115 120 125	
ctg gta tac ttg ttc tac atg tct aag tac gtg gaa ttc atg gat acc	489
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr	
130 135 140	
gtt atc atg ata ctg aag cgc agc acc agg caa ata agc ttc ctc cac	537
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His	
145 150 155 160	
gtt tat cat cat tct tca att tcc ctc att tgg tgg gct att gct cat	585
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His	
165 170 175	
cac gct cct ggc ggt gaa gca tat tgg tct gcg gct ctg aac tca gga	633
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly	
180 185 190	
gtg cat gtt ctc atg tat gcg tat tac ttc ttg gct gcc tgc ctt cga	681
Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg	
195 200 205	
agt agc cca aag tta aaa aat aag tac ctt ttt tgg ggc agg tac ttg	729
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu	
210 215 220	
aca caa ttc caa atg ttc cag ttt atg ctg aac tta gtg cag gct tac	777
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr	
225 230 235 240	
tac gac atg aaa acg aat gcg cca tat cca caa tgg ctg atc aag att	825

Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile  
                   245                                  250                                  255

ttg ttc tac tac atg atc tcg ttg ctg ttt ctt ttc ggc aat ttt tac 873  
 Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr  
                   260                                  265                                  270

gta caa aaa tac atc aaa ccc tct gac gga aag caa aag gga gct aaa 921  
 Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys  
                   275                                  280                                  285

act gag tga gctgtatcaa gccatagaaa ctctattatg ttagaacctg 970  
 Thr Glu  
                   290

aagttggtgc tttcttatct ccacttatct ttttaagcagc atcagttttg aaatgatgtg 1030

tgggcgtggt ctgcaagtag tcatcaatat aatcggcctg agcacttcag atggattgtt 1090

agaacatgag taaaagcggg tattacgggtg tttattttgt accaaatcac cgcacgggtg 1150

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<210> 4

<211> 290

<212> PRT

<213> Physcomitrella patens

<400> 4

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                   20                                  25                                  30

Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile  
           35                                  40                                  45

Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu

50

55

60

Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu  
65 70 75 80

Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser  
85 90 95

Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr  
100 105 110

Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile  
115 120 125

Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr  
130 135 140

Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His  
145 150 155 160

Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His  
165 170 175

His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly  
180 185 190

Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg  
195 200 205

Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu  
210 215 220

Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr  
225 230 235 240

Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile  
245 250 255

Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr  
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Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys  
 275 280 285

Thr Glu  
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<210> 5

<211> 1054

<212> DNA

<213> Thraustochytrium

<220>

<221> CDS

<222> (43)..(858)

<223> Δ6-elongase

<400> 5

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tcg gcg gcc ttc aag tgg caa gtc acg tac gac gcc aag gac agc ttc 150  
 Ser Ala Ala Phe Lys Trp Gln Val Thr Tyr Asp Ala Lys Asp Ser Phe  
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gtc ggg ccc ctg gga atc cgg gag ccg ctc ggg ctc ctg gtg ggc tcc 198  
 Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu Leu Val Gly Ser  
 40 45 50

gtg gtc ctc tac ctg agc ctg ctg gcc gtg gtc tac gcg ctg cgg aac 246  
 Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr Ala Leu Arg Asn  
 55 60 65

tac ctt ggc ggc ctc atg gcg ctc cgc agc gtg cat aac ctc ggg ctc 294

Tyr	Leu	Gly	Gly	Leu	Met	Ala	Leu	Arg	Ser	Val	His	Asn	Leu	Gly	Leu		
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tgc	ctc	ttc	tcg	ggc	gcc	gtg	tgg	atc	tac	acg	agc	tac	ctc	atg	atc	342	
Cys	Leu	Phe	Ser	Gly	Ala	Val	Trp	Ile	Tyr	Thr	Ser	Tyr	Leu	Met	Ile		
85					90				95						100		
cag	gat	ggg	cac	ttt	cgc	agc	ctc	gag	gcg	gca	acg	tgc	gag	ccg	ctc	390	
Gln	Asp	Gly	His	Phe	Arg	Ser	Leu	Glu	Ala	Ala	Thr	Cys	Glu	Pro	Leu		
			105						110						115		
aag	cat	ccg	cac	ttc	cag	ctc	atc	agc	ttg	ctc	ttt	gcg	ctg	tcc	aag	438	
Lys	His	Pro	His	Phe	Gln	Leu	Ile	Ser	Leu	Leu	Phe	Ala	Leu	Ser	Lys		
			120					125							130		
atc	tgg	gag	tgg	ttc	gac	acg	gtg	ctc	ctc	atc	gtc	aag	ggc	aac	aag	486	
Ile	Trp	Glu	Trp	Phe	Asp	Thr	Val	Leu	Leu	Ile	Val	Lys	Gly	Asn	Lys		
		135					140								145		
ctc	cgc	ttc	ctg	cac	gtc	ttg	cac	cac	gcc	acg	acc	ttt	tgg	ctc	tac	534	
Leu	Arg	Phe	Leu	His	Val	Leu	His	His	Ala	Thr	Thr	Phe	Trp	Leu	Tyr		
		150					155								160		
gcc	atc	gac	cac	atc	ttt	ctc	tcg	tcc	atc	aag	tac	ggc	gtc	gcg	gtc	582	
Ala	Ile	Asp	His	Ile	Phe	Leu	Ser	Ser	Ile	Lys	Tyr	Gly	Val	Ala	Val		
165						170				175					180		
aat	gct	ttc	atc	cac	acc	gtc	atg	tac	gcg	cac	tac	ttc	cgc	cca	ttc	630	
Asn	Ala	Phe	Ile	His	Thr	Val	Met	Tyr	Ala	His	Tyr	Phe	Arg	Pro	Phe		
				185					190						195		
ccg	aag	ggc	ttg	cgc	ccg	ctt	att	acg	cag	ttg	cag	atc	gtc	cag	ttc	678	
Pro	Lys	Gly	Leu	Arg	Pro	Leu	Ile	Thr	Gln	Leu	Gln	Ile	Val	Gln	Phe		
			200						205						210		
att	ttc	agc	atc	ggc	atc	cat	acc	gcc	att	tac	tgg	cac	tac	gac	tgc	726	
Ile	Phe	Ser	Ile	Gly	Ile	His	Thr	Ala	Ile	Tyr	Trp	His	Tyr	Asp	Cys		
			215					220							225		
gag	ccg	ctc	gtg	cat	acc	cac	ttt	tgg	gaa	tac	gtc	acg	ccc	tac	ctt	774	



13

Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val Thr Pro Tyr Leu  
 230 235 240

ttc gtc gtg ccc ttc ctc atc ctc ttt ttc aat ttt tac ctg cag cag 822  
 Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe Tyr Leu Gln Gln  
 245 250 255 260

tac gtc ctc gcg ccc gca aaa acc aag aag gca tag ccacgtaaca 868  
 Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala  
 265 270

gtagaccagc agcgccgagg acgcgtgccg cgttatcgcg aagcacgaaa taaagaagat 928

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1048

ctcgag 1054

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<211> 271

<212> PRT

<213> Thraustochytrium

<400> 6

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Arg Tyr Ala Ser Ser Ala Ala Phe Lys Trp Gln Val Thr Tyr Asp Ala  
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Lys Asp Ser Phe Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu  
 35 40 45

Leu Val Gly Ser Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr  
 50 55 60

Ala Leu Arg Asn Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His  
 65 70 75 80

Asn Leu Gly Leu Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser  
85 90 95

Tyr Leu Met Ile Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr  
100 105 110

Cys Glu Pro Leu Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe  
115 120 125

Ala Leu Ser Lys Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val  
130 135 140

Lys Gly Asn Lys Leu Arg Phe Leu His Val Leu His His Ala Thr Thr  
145 150 155 160

Phe Trp Leu Tyr Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr  
165 170 175

Gly Val Ala Val Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr  
180 185 190

Phe Arg Pro Phe Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln  
195 200 205

Ile Val Gln Phe Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp  
210 215 220

His Tyr Asp Cys Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val  
225 230 235 240

Thr Pro Tyr Leu Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe  
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Tyr Leu Gln Gln Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala  
260 265 270

<210> 7

<211> 2040

&lt;212&gt; DNA

<213> *Ceratodon purpureus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (176)..(1627)

<223>  $\Delta 6$ -desaturase

&lt;400&gt; 7

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tcagggtcga tcaggttatt ctgaaaaagg ctgcgtctgt gagcagtttg caaaa atg 178

Met

1

gcc ctc gtt acc gac ttt ctg aac ttt ctg ggc acg aca tgg agc aag 226

Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser Lys

5

10

15

tac agc gtg tac acc cat agc tat gct gga aac tat ggg cct act ttg 274

Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr Leu

20

25

30

aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg gga cag aca 322

Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln Thr

35

40

45

ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act tac tct ctg 370

Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser Leu

50

55

60

65

gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg atg atc gtc 418

Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile Val

70

75

80

aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac cac cct gga 466

Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro Gly

85

90

95

ggg acg gta att agc acc tac ttt ggg cgg gat ggc aca gac gtt ttc	514
Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe	
100 105 110	
gca aca ttc cat cca cct gcc gca tgg aag caa ctc aat gac tac tac	562
Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn Asp Tyr Tyr	
115 120 125	
att gga gac ctt gct agg gaa gag ccc ctt gat gaa ttg ctt aaa gac	610
Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu Leu Lys Asp	
130 135 140 145	
tac aga gat atg aga gcc gag ttt gtt aga gaa ggg ctt ttc aag agt	658
Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu Phe Lys Ser	
150 155 160	
tcc aag gcc tgg ttc ctg ctt cag act ctg att aat gca gct ctc ttt	706
Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala Ala Leu Phe	
165 170 175	
gct gcg agc att gcg act atc tgt tac gac aag agt tac tgg gct att	754
Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr Trp Ala Ile	
180 185 190	
gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag tgt gga tgg	802
Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly Trp	
195 200 205	
ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac cgt acc gcg	850
Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr Ala	
210 215 220 225	
aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt ggc ttt agt	898
Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe Ser	
230 235 240	
gta tca tgg tgg agg acg aag cac aac att cat cat act gct ccg aat	946
Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro Asn	
245 250 255	

gag tgc gac gaa cag tac aca cct cta gac gaa gac att gat act ctc	994
Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile Asp Thr Leu	
260 265 270	
ccc atc att gcc tgg agc aag gaa att ttg gcc acc gtt gag agc aag	1042
Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val Glu Ser Lys	
275 280 285	
aga att ttg cga gtg ctt caa tat cag cac tac atg att ctg cct cta	1090
Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile Leu Pro Leu	
290 295 300 305	
ttg ttc atg gcc cgg tac agt tgg act ttt gga agt ttg ctc ttc aca	1138
Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu Leu Phe Thr	
310 315 320	
ttc aat cct gat ttg agc acg acc aag gga ttg ata gag aag gga aca	1186
Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu Lys Gly Thr	
325 330 335	
gtt gct ttt cac tac gcc tgg ttc agt tgg gct gcg ttc cat att ttg	1234
Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe His Ile Leu	
340 345 350	
ccg ggt gtc gct aag cct ctt gcg tgg atg gta gca act gag ctt gtg	1282
Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr Glu Leu Val	
355 360 365	
gcc ggt ttg ttg ttg gga ttc gtg ttt acg ttg agt cac aat gga aag	1330
Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly Lys	
370 375 380 385	
gag gtt tac aat gaa tcg aag gac ttc gtg aga gcc cag gtt att acc	1378
Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile Thr	
390 395 400	
acc cgt aac acc aag cga ggc tgg ttc aac gat tgg ttc act ggg gga	1426
Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly Gly	
405 410 415	

ctc gac acc cag att gag cat cac ctg ttt cca aca atg ccc agg cac 1474  
 Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His  
           420                          425                          430

aac tac ccc aag atc gca cct cag gtc gag gct ctt tgc aag aag cac 1522  
 Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys His  
           435                          440                          445

ggc ctc gag tac gat aat gtc tcc gtc gtt ggt gcc tct gtc gcg gtt 1570  
 Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala Val  
 450                          455                          460                          465

gtg aag gcg ctc aag gaa att gct gat gaa gcg tca att cgg ctt cac 1618  
 Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu His  
                           470                          475                          480

gct cac taa gaaatcgctg aactttgact attcattttt ttgcctggc 1667  
 Ala His

tacctcaaat gttcgggagc aggtgcttgg cagtgtgttc aaccggagcg cactgaaaat 1727

gtgcagaatc catttccaga aattaccatt cctagctaaa tcttcttttt accaggctcg 1787

atatatgaaa cttttttgat gcaacaagta gcattcaatt gaagacattg ttcgagatat 1847

aattcgcagt gtttctattc agcgggcata cgtactagtc catatcggcg gttgccgaga 1907

gtttacatta ttagttggca caacgagtag atctagtgtg aatttctatt tccgcatgta 1967

atattactct gaatatatac cgttatctat tttcctaaaa aaaaaaaaaa aaaaaaaaaa 2027

aaaaaaaaaa aaa 2040

<210> 8

<211> 483

<212> PRT

<213> Ceratodon purpureus

&lt;400&gt; 8

Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser  
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Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr  
 20 25 30

Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln  
 35 40 45

Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser  
 50 55 60

Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile  
 65 70 75 80

Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro  
 85 90 95

Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val  
 100 105 110

Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn Asp Tyr  
 115 120 125

Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu Leu Lys  
 130 135 140

Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu Phe Lys  
 145 150 155 160

Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala Ala Leu  
 165 170 175

Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr Trp Ala  
 180 185 190

Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly  
 195 200 205

Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr  
 210 215 220

Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe  
 225 230 235 240

Ser Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro  
 245 250 255

Asn Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile Asp Thr  
 260 265 270

Leu Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val Glu Ser  
 275 280 285

Lys Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile Leu Pro  
 290 295 300

Leu Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu Leu Phe  
 305 310 315 320

Thr Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu Lys Gly  
 325 330 335

Thr Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe His Ile  
 340 345 350

Leu Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr Glu Leu  
 355 360 365

Val Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly  
 370 375 380

Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile  
 385 390 395 400

Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly  
 405 410 415

Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg



420

425

430

His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys  
 435 440 445

His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala  
 450 455 460

Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu  
 465 470 475 480

His Ala His

<210> 9

<211> 1467

<212> DNA

<213> Ceratodon purpureus

<220>

<221> CDS

<222> (10)..(1461)

<223> Δ6-desaturase

<400> 9

ggatccaaa atg gcc ctc gtt acc gac ttt ctg aac ttt ctg ggc acg aca 51  
 Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr  
 1 5 10

tgg agc aag tac agc gtg tac acc cat agc tat gct gga aac tat ggg 99  
 Trp Ser Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly  
 15 20 25 30

cct act ttg aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg 147  
 Pro Thr Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala  
 35 40 45

gga cag aca ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act 195  
 Gly Gln Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr  
 50 55 60

tac tct ctg gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg	243
Tyr Ser Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp	
65 70 75	
atg atc gtc aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac	291
Met Ile Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp	
80 85 90	
cac cct gga ggg acg gta att agc acc tac ttt ggg cgg gat ggc aca	339
His Pro Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr	
95 100 105 110	
gac gtt ttc gca aca ttc cat cca cct gcc gca tgg aag caa ctc aat	387
Asp Val Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn	
115 120 125	
gac tac tac att gga gac ctt gct agg gaa gag ccc ctt gat gaa ttg	435
Asp Tyr Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu	
130 135 140	
ctt aaa gac tac aga gat atg aga gcc gag ttt gtt aga gaa ggg ctt	483
Leu Lys Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu	
145 150 155	
ttc aag agt tcc aag gcc tgg ttc ctg ctt cag act ctg att aat gca	531
Phe Lys Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala	
160 165 170	
gct ctc ttt gct gcg agc att gcg act atc tgt tac gac aag agt tac	579
Ala Leu Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr	
175 180 185 190	
tgg gct att gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag	627
Trp Ala Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln	
195 200 205	
tgt gga tgg ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac	675
Cys Gly Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn	
210 215 220	

cgt acc gcg aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt	723
Arg Thr Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu	
225 230 235	
ggc ttt agt gta tca tgg tgg agg acg aag cac aac att cat cat act	771
Gly Phe Ser Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr	
240 245 250	
gct ccg aat gag tgc gac gaa cag tac aca cct cta gac gaa gac att	819
Ala Pro Asn Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile	
255 260 265 270	
gat act ctc ccc atc att gcc tgg agc aag gaa att ttg gcc acc gtt	867
Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val	
275 280 285	
gag agc aag aga att ttg cga gtg ctt caa tat cag cac tac atg att	915
Glu Ser Lys Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile	
290 295 300	
ctg cct cta ttg ttc atg gcc cgg tac agt tgg act ttt gga agt ttg	963
Leu Pro Leu Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu	
305 310 315	
ctc ttc aca ttc aat cct gat ttg agc acg acc aag gga ttg ata gag	1011
Leu Phe Thr Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu	
320 325 330	
aag gga aca gtt gct ttt cac tac gcc tgg ttc agt tgg gct gcg ttc	1059
Lys Gly Thr Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe	
335 340 345 350	
cat att ttg ccg ggt gtc gct aag cct ctt gcg tgg atg gta gca act	1107
His Ile Leu Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr	
355 360 365	
gag ctt gtg gcc ggt ttg ttg ttg gga ttc gtg ttt acg ttg agt cac	1155
Glu Leu Val Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His	
370 375 380	

aat gga aag gag gtt tac aat gaa tcg aag gac ttc gtg aga gcc cag 1203  
 Asn Gly Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln  
 385 390 395

gtt att acc acc cgt aac acc aag cga ggc tgg ttc aac gat tgg ttc 1251  
 Val Ile Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe  
 400 405 410

act ggg gga ctc gac acc cag att gag cat cac ctg ttt cca aca atg 1299  
 Thr Gly Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met  
 415 420 425 430

ccc agg cac aac tac ccc aag atc gca cct cag gtc gag gct ctt tgc 1347  
 Pro Arg His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys  
 435 440 445

aag aag cac ggc ctc gag tac gat aat gtc tcc gtc gtt ggt gcc tct 1395  
 Lys Lys His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser  
 450 455 460

gtc gcg gtt gtg aag gcg ctc aag gaa att gct gat gaa gcg tca att 1443  
 Val Ala Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile  
 465 470 475

cgg ctt cac gct cac taa gtcgac 1467  
 Arg Leu His Ala His  
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<210> 10

<211> 483

<212> PRT

<213> Ceratodon purpureus

<400> 10

Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser  
 1 5 10 15

Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr

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25

30

Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln  
 35 40 45

Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser  
 50 55 60

Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile  
 65 70 75 80

Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro  
 85 90 95

Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val  
 100 105 110

Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn Asp Tyr  
 115 120 125

Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu Leu Lys  
 130 135 140

Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu Phe Lys  
 145 150 155 160

Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala Ala Leu  
 165 170 175

Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr Trp Ala  
 180 185 190

Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly  
 195 200 205

Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr  
 210 215 220

Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe  
 225 230 235 240

Ser Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro  
245 250 255

Asn Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile Asp Thr  
260 265 270

Leu Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val Glu Ser  
275 280 285

Lys Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile Leu Pro  
290 295 300

Leu Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu Leu Phe  
305 310 315 320

Thr Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu Lys Gly  
325 330 335

Thr Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe His Ile  
340 345 350

Leu Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr Glu Leu  
355 360 365

Val Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly  
370 375 380

Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile  
385                      390                      395                      400

Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly  
405 410 415

Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg  
420 425 430

His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys  
435 440 445

His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala  
 450 455 460

Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu  
 465 470 475 480

His Ala His

<210> 11

<211> 2160

<212> DNA

<213> *Ceratodon purpureus*

<220>

<221> CDS

<222> (159)..(1721)

<223>  $\Delta 6$ -desaturase

<400> 11

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tttcgtgggtt ttggcggttg cattgcgcga gggcggacag tgggagtgcg ggaggtctgt 120

ttgtgcatga cgaggtgggt gtaatcttcg ccggcaga atg gtg tcc cag ggc ggc 176

Met Val Ser Gln Gly Gly

1

5

ggg ctc tcg cag ggt tcc att gaa gaa aac att gac gtt gag cac ttg 224

Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn Ile Asp Val Glu His Leu

10

15

20

gca acg atg ccc ctc gtc agt gac ttc cta aat gtc ctg gga acg act. 272

Ala Thr Met Pro Leu Val Ser Asp Phe Leu Asn Val Leu Gly Thr Thr

25

30

35

ttg ggc cag tgg agt ctt tcc act aca ttc gct ttc aag agg ctc acg. 320

Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe Ala Phe Lys Arg Leu Thr

40

45

50

act aag aaa cac agt tcg gac atc tcg gtg gag gca caa aaa gaa tcg 368  
 Thr Lys Lys His Ser Ser Asp Ile Ser Val Glu Ala Gln Lys Glu Ser  
 55 60 65 70

gtt gcg cgg ggg cca gtt gag aat att tct caa tcg gtt gcg cag ccc 416  
 Val Ala Arg Gly Pro Val Glu Asn Ile Ser Gln Ser Val Ala Gln Pro  
 75 80 85

atc agg cgg agg tgg gtg cag gat aaa aag ccg gtt act tac agc ctg 464  
 Ile Arg Arg Arg Trp Val Gln Asp Lys Lys Pro Val Thr Tyr Ser Leu  
 90 95 100

aag gat gta gct tcg cac gat atg ccc cag gac tgc tgg att ata atc 512  
 Lys Asp Val Ala Ser His Asp Met Pro Gln Asp Cys Trp Ile Ile Ile  
 105 110 115

aaa gag aag gtg tat gat gtg agc acc ttc gct gag cag cac cct gga 560  
 Lys Glu Lys Val Tyr Asp Val Ser Thr Phe Ala Glu Gln His Pro Gly  
 120 125 130

ggc acg gtt atc aac acc tac ttc gga cga gac gcc aca gat gtt ttc 608  
 Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg Asp Ala Thr Asp Val Phe  
 135 140 145 150

tct act ttc cac gca tcc acc tca tgg aag att ctt cag aat ttc tac 656  
 Ser Thr Phe His Ala Ser Thr Ser Trp Lys Ile Leu Gln Asn Phe Tyr  
 155 160 165

atc ggg aac ctt gtt agg gag gag ccg act ttg gag ctg ctg aag gag 704  
 Ile Gly Asn Leu Val Arg Glu Glu Pro Thr Leu Glu Leu Leu Lys Glu  
 170 175 180

tac aga gag ttg aga gcc ctt ttc ttg aga gaa cag ctt ttc aag agt 752  
 Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser  
 185 190 195

tcc aaa tcc tac tac ctt ttc aag act ctc ata aat gtt tcc att gtt 800  
 Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu Ile Asn Val Ser Ile Val  
 200 205 210



gcc aca agc att gcg ata atc agt ctg tac aag tct tac cgg gcg gtt	848
Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr Lys Ser Tyr Arg Ala Val	
215 220 225 230	
ctg tta tca gcc agt ttg atg ggc ttg ttt att caa cag tgc gga tgg	896
Leu Leu Ser Ala Ser Leu Met Gly Leu Phe Ile Gln Gln Cys Gly Trp	
235 240 245	
ttg tct cac gat ttt cta cac cat cag gta ttt gag aca cgc tgg ctc	944
Leu Ser His Asp Phe Leu His His Gln Val Phe Glu Thr Arg Trp Leu	
250 255 260	
aat gac gtt gtt ggc tat gtg gtc ggc aac gtt gtt ctg gga ttc agt	992
Asn Asp Val Val Gly Tyr Val Val Gly Asn Val Val Leu Gly Phe Ser	
265 270 275	
gtc tcg tgg tgg aag acc aag cac aac ctg cat cat gct gct ccg aat	1040
Val Ser Trp Trp Lys Thr Lys His Asn Leu His His Ala Ala Pro Asn	
280 285 290	
gaa tgc gac caa aag tac aca ccg att gat gag gat att gat act ctc	1088
Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp Glu Asp Ile Asp Thr Leu	
295 300 305 310	
ccc atc att gct tgg agt aaa gat ctc ttg gcc act gtt gag agc aag	1136
Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu Ala Thr Val Glu Ser Lys	
315 320 325	
acc atg ttg cga gtt ctt cag tac cag cac cta ttc ttt ttg gtt ctt	1184
Thr Met Leu Arg Val Leu Gln Tyr Gln His Leu Phe Phe Leu Val Leu	
330 335 340	
ttg acg ttt gcc cgg gcg agt tgg cta ttt tgg agc gcg gcc ttc act	1232
Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe Trp Ser Ala Ala Phe Thr	
345 350 355	
ctc agg ccc gag ttg acc ctt ggc gag aag ctt ttg gag agg gga acg	1280
Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys Leu Leu Glu Arg Gly Thr	
360 365 370	

atg gct ttg cac tac att tgg ttt aat agt gtt gcg ttt tat ctg ctc	1328
Met Ala Leu His Tyr Ile Trp Phe Asn Ser Val Ala Phe Tyr Leu Leu	
375                      380                      385                      390	
ccc gga tgg aaa cca gtt gta tgg atg gtg gtc agc gag ctc atg tct	1376
Pro Gly Trp Lys Pro Val Val Trp Met Val Val Ser Glu Leu Met Ser	
395                      400                      405	
ggt ttc ctg ctg gga tac gta ttt gta ctc agt cac aat gga atg gag	1424
Gly Phe Leu Leu Gly Tyr Val Phe Val Leu Ser His Asn Gly Met Glu	
410                      415                      420	
gtg tac aat acg tca aag gac ttc gtg aat gcc cag att gca tcg act	1472
Val Tyr Asn Thr Ser Lys Asp Phe Val Asn Ala Gln Ile Ala Ser Thr	
425                      430                      435	
cgc gac atc aaa gca ggg gtg ttt aat gat tgg ttc acc gga ggt ctc	1520
Arg Asp Ile Lys Ala Gly Val Phe Asn Asp Trp Phe Thr Gly Gly Leu	
440                      445                      450	
aac aga cag att gag cat cat cta ttt cca acg atg ccc agg cac aac	1568
Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn	
455                      460                      465                      470	
ctt aat aaa att tct cct cac gtg gag act ttg tgc aag aag cat gga	1616
Leu Asn Lys Ile Ser Pro His Val Glu Thr Leu Cys Lys Lys His Gly	
475                      480                      485	
ctg gtc tac gaa gac gtg agc atg gct tcg ggc act tac cgg gtt ttg	1664
Leu Val Tyr Glu Asp Val Ser Met Ala Ser Gly Thr Tyr Arg Val Leu	
490                      495                      500	
aaa aca ctt aag gac gtt gcc gat gct gct tca cac cag cag ctt gct	1712
Lys Thr Leu Lys Asp Val Ala Asp Ala Ala Ser His Gln Gln Leu Ala	
505                      510                      515	
gcg agt tga ggcatcgtag cactcgtag aacatttttg tctgttatag	1761
Ala Ser	
520	

tggtcatatg tgatcgaggg gaaaagggtcc catgctctga tctattcttc tgtagccaat 1821  
 atttttcaat tgaaaggagg ttcctcactt atcttccatc tatcgttgca catcctgcat 1881  
 cagagttagc gttggagtaa tgtaagcac ttgtagatta tgcccacat tgccacattt 1941  
 ctgttcggtt acaatcgttt gattccatgc taccctcgt gttcatctcg ttgttataag 2001  
 caagcttgaa aaaacatgct acgagattgg cagacgttgt cttggcagct gtagagggtg 2061  
 gttccattca ttgtgtagta cagaactctc tcgtccctgt ttctctacat tacttggtac 2121  
 atagtgactt tcattcacag caaaaaaaaaa aaaaaaaaaa 2160

&lt;210&gt; 12

&lt;211&gt; 520

&lt;212&gt; PRT

<213> *Ceratodon purpureus*

&lt;400&gt; 12

Met Val Ser Gln Gly Gly Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn  
 1 5 10 15

Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu  
 20 25 30

Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe  
 35 40 45

Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val  
 50 55 60

Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser  
 65 70 75 80

Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys  
 85 90 95

Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln

100

105

110

Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe  
 115 120 125

Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg  
 130 135 140

Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys  
 145 150 155 160

Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr  
 165 170 175

Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg  
 180 185 190

Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu  
 195 200 205

Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr  
 210 215 220

Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe  
 225 230 235 240

Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val  
 245 250 255

Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn  
 260 265 270

Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu  
 275 280 285

His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp  
 290 295 300

Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu  
 305 310 315 320

Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His  
 325 330 335

Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe  
 340 345 350

Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys  
 355 360 365

Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser  
 370 375 380

Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val  
 385 390 395 400

Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu  
 405 410 415

Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn  
 420 425 430

Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp  
 435 440 445

Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro  
 450 455 460

Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr  
 465 470 475 480

Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser  
 485 490 495

Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala  
 500 505 510

Ser His Gln Gln Leu Ala Ala Ser  
 515 520

&lt;210&gt; 13

&lt;211&gt; 1434

&lt;212&gt; DNA

<213> *Phaeodactylum tricornutum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1434)

<223>  $\Delta 6$ -desaturase

&lt;400&gt; 13

atg ggc aaa gga ggg gac gct cgg gcc tcg aag ggc tca acg gcg gct	48
Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala	
1 5 10 15	
cgc aag atc agt tgg cag gaa gtc aag acc cac gcg tct ccg gag gac	96
Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp	
20 25 30	
gcc tgg atc att cac tcc aat aag gtc tac gac gtg tcc aac tgg cac	144
Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His	
35 40 45	
gaa cat ccc gga ggc gcc gtc att ttc acg cac gcc ggt gac gac atg	192
Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met	
50 55 60	
acg gac att ttc gct gcc ttt cac gca ccc gga tcg cag tcg ctc atg	240
Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met	
65 70 75 80	
aag aag ttc tac att ggc gaa ttg ctc ccg gaa acc acc ggc aag gag	288
Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu	
85 90 95	
ccg cag caa atc gcc ttt gaa aag ggc tac cgc gat ctg cgc tcc aaa	336
Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys	
100 105 110	

ctc atc atg atg ggc atg ttc aag tcc aac aag tgg ttc tac gtc tac	384
Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr	
115 120 125	
aag tgc ctc agc aac atg gcc att tgg gcc gcc gcc tgt gct ctc gtc	432
Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val	
130 135 140	
ttt tac tcg gac cgc ttc tgg gta cac ctg gcc agc gcc gtc atg ctg	480
Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu	
145 150 155 160	
gga aca ttc ttt cag cag tcg gga tgg ttg gca cac gac ttt ctg cac	528
Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His	
165 170 175	
cac cag gtc ttc acc aag cgc aag cac ggg gat ctc gga gga ctc ttt	576
His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe	
180 185 190	
tgg ggg aac ctc atg cag ggt tac tcc gta cag tgg tgg aaa aac aag	624
Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys	
195 200 205	
cac aac gga cac cac gcc gtc ccc aac ctc cac tgc tcc tcc gca gtc	672
His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val	
210 215 220	
gcg caa gat ggg gac ccg gac atc gat acc atg ccc ctt ctc gcc tgg	720
Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp	
225 230 235 240	
tcc gtc cag caa gcc cag tct tac cgg gaa ctc caa gcc gac gga aag	768
Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala Asp Gly Lys	
245 250 255	
gat tcg ggt ttg gtc aag ttc atg atc cgt aac caa tcc tac ttt tac	816
Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr	
260 265 270	

ttt ccc atc ttg ttg ctc gcc cgc ctg tcg tgg ttg aac gag tcc ttc	864
Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe	
275 280 285	
aag tgc gcc ttt ggg ctt gga gct gcg tcg gag aac gct gct ctc gaa	912
Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu	
290 295 300	
ctc aag gcc aag ggt ctt cag tac ccc ctt ttg gaa aag gct ggc atc	960
Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys Ala Gly Ile	
305 310 315 320	
ctg ctg cac tac gct tgg atg ctt aca gtt tcg tcc ggc ttt gga cgc	1008
Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly Phe Gly Arg	
325 330 335	
ttc tcg ttc gcg tac acc gca ttt tac ttt cta acc gcg acc gcg tcc	1056
Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser	
340 345 350	
tgt gga ttc ttg ctc gcc att gtc ttt ggc ctc ggc cac aac ggc atg	1104
Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met	
355 360 365	
gcc acc tac aat gcc gac gcc cgt ccg gac ttc tgg aag ctc caa gtc	1152
Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val	
370 375 380	
acc acg act cgc aac gtc acg ggc gga cac ggt ttc ccc caa gcc ttt	1200
Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe	
385 390 395 400	
gtc gac tgg ttc tgt ggt ggc ctc cag tac caa gtc gac cac cac tta	1248
Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu	
405 410 415	
ttc ccc agc ctg ccc cga cac aat ctg gcc aag aca cac gca ctg gtc	1296
Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val	
420 425 430	



gaa tcg ttc tgc aag gag tgg ggt gtc cag tac cac gaa gcc gac ctt 1344  
 Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu  
 435 440 445

gtg gac ggg acc atg gaa gtc ttg cac cat ttg ggc agc gtg gcc ggc 1392  
 Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly  
 450 455 460

gaa ttc gtc gtg gat ttt gta cgc gat gga ccc gcc atg taa 1434  
 Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met  
 465 470 475

<210> 14

<211> 477

<212> PRT

<213> Phaeodactylum tricornutum

<400> 14

Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala  
 1 5 10 15

Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp  
 20 25 30

Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His  
 35 40 45

Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met  
 50 55 60

Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met  
 65 70 75 80

Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu  
 85 90 95

Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys  
 100 105 110

Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr  
 115 120 125

Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val  
 130 135 140

Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu  
 145 150 155 160

Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His  
 165 170 175

His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe  
 180 185 190

Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys  
 195 200 205

His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val  
 210 215 220

Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp  
 225 230 235 240

Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala Asp Gly Lys  
 245 250 255

Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr  
 260 265 270

Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe  
 275 280 285

Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu  
 290 295 300

Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys Ala Gly Ile  
 305 310 315 320

Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly Phe Gly Arg

325

330

335

Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser  
 340 345 350

Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met  
 355 360 365

Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val  
 370 375 380

Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe  
 385 390 395 400

Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu  
 405 410 415

Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val  
 420 425 430

Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu  
 435 440 445

Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly  
 450 455 460

Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met  
 465 470 475

&lt;210&gt; 15

&lt;211&gt; 1563

&lt;212&gt; DNA

&lt;213&gt; Ceratodon purpureus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1563)

&lt;223&gt; Δ6-desaturase

&lt;400&gt; 15

atg gtg tcc cag ggc ggc ggt ctc tcg cag ggt tcc att gaa gaa aac	48
Met Val Ser Gln Gly Gly Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn	
1 5 10 15	
att gac gtt gag cac ttg gca acg atg ccc ctc gtc agt gac ttc cta	96
Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu	
20 25 30	
aat gtc ctg gga acg act ttg ggc cag tgg agt ctt tcc act aca ttc	144
Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe	
35 40 45	
gct ttc aag agg ctc acg act aag aaa cac agt tcg gac atc tcg gtg	192
Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val	
50 55 60	
gag gca caa aaa gaa tcg gtt gcg cgg ggg cca gtt gag aat att tct	240
Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser	
65 70 75 80	
caa tcg gtt gcg cag ccc atc agg cgg agg tgg gtg cag gat aaa aag	288
Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys	
85 90 95	
ccg gtt act tac agc ctg aag gat gta gct tcg cac gat atg ccc cag	336
Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln	
100 105 110	
gac tgc tgg att ata atc aaa gag aag gtg tat gat gtg agc acc ttc	384
Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe	
115 120 125	
gct gag cag cac cct gga ggc acg gtt atc aac acc tac ttc gga cga	432
Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg	
130 135 140	
gac gcc aca gat gtt ttc tct act ttc cac gca tcc acc tca tgg aag	480
Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys	
145 150 155 160	

att ctt cag aat ttc tac atc ggg aac ctt gtt agg gag gag ccg act	528
Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr	
165 170 175	
ttg gag ctg ctg aag gag tac aga gag ttg aga gcc ctt ttc ttg aga	576
Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg	
180 185 190	
gaa cag ctt ttc aag agt tcc aaa tcc tac tac ctt ttc aag act ctc	624
Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu	
195 200 205	
ata aat gtt tcc att gtt gcc aca agc att gcg ata atc agt ctg tac	672
Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr	
210 215 220	
aag tct tac cgg gcg gtt ctg tta tca gcc agt ttg atg ggc ttg ttt	720
Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe	
225 230 235 240	
att caa cag tgc gga tgg ttg tct cac gat ttt cta cac cat cag gta	768
Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val	
245 250 255	
ttt gag aca cgc tgg ctc aat gac gtt gtt ggc tat gtg gtc ggc aac	816
Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn	
260 265 270	
gtt gtt ctg gga ttc agt gtc tcg tgg tgg aag acc aag cac aac ctg	864
Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu	
275 280 285	
cat cat gct gct ccg aat gaa tgc gac caa aag tac aca ccg att gat	912
His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp	
290 295 300	
gag gat att gat act ctc ccc atc att gct tgg agt aaa gat ctc ttg	960
Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu	
305 310 315 320	

gcc act gtt gag agc aag acc atg ttg cga gtt ctt cag tac cag cac	1008
Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His	
325 330 335	
cta ttc ttt ttg gtt ctt ttg acg ttt gcc cgg gcg agt tgg cta ttt	1056
Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe	
340 345 350	
tgg agc gcg gcc ttc act ctc agg ccc gag ttg acc ctt ggc gag aag	1104
Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys	
355 360 365	
ctt ttg gag agg gga acg atg gct ttg cac tac att tgg ttt aat agt	1152
Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser	
370 375 380	
gtt gcg ttt tat ctg ctc ccc gga tgg aaa cca gtt gta tgg atg gtg	1200
Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val	
385 390 395 400	
gtc agc gag ctc atg tct ggt ttc ctg ctg gga tac gta ttt gta ctc	1248
Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu	
405 410 415	
agt cac aat gga atg gag gtg tac aat acg tca aag gac ttc gtg aat	1296
Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn	
420 425 430	
gcc cag att gca tcg act cgc gac atc aaa gca ggg gtg ttt aat gat	1344
Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp	
435 440 445	
tgg ttc acc gga ggt ctc aac aga cag att gag cat cat cta ttt cca	1392
Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro	
450 455 460	
acg atg ccc agg cac aac ctt aat aaa att tct cct cac gtg gag act	1440
Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr	
465 470 475 480	

ttg tgc aag aag cat gga ctg gtc tac gaa gac gtg agc atg gct tcg 1488  
 Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser  
 485 490 495

ggc act tac cgg gtt ttg aaa aca ctt aag gac gtt gcc gat gct gct 1536  
 Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala  
 500 505 510

tca cac cag cag ctt gct gcg agt tga 1563  
 Ser His Gln Gln Leu Ala Ala Ser  
 515 520

<210> 16

<211> 520

<212> PRT

<213> Ceratodon purpureus

<400> 16

Met Val Ser Gln Gly Gly Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn  
 1 5 10 15

Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu  
 20 25 30

Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe  
 35 40 45

Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val  
 50 55 60

Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser  
 65 70 75 80

Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys  
 85 90 95

Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln  
 100 105 110

Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe  
 115 120 125

Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg  
 130 135 140

Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys  
 145 150 155 160

Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr  
 165 170 175

Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg  
 180 185 190

Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu  
 195 200 205

Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr  
 210 215 220

Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe  
 225 230 235 240

Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val  
 245 250 255

Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn  
 260 265 270

Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu  
 275 280 285

His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp  
 290 295 300

Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu  
 305 310 315 320



Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His  
 325 330 335

Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe  
 340 345 350

Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys  
 355 360 365

Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser  
 370 375 380

Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val  
 385 390 395 400

Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu  
 405 410 415

Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn  
 420 425 430

Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp  
 435 440 445

Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro  
 450 455 460

Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr  
 465 470 475 480

Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser  
 485 490 495

Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala  
 500 505 510

Ser His Gln Gln Leu Ala Ala Ser  
 515 520

cac aac aag cca agc gat tgc tgg att gtt gta aaa aac aag gtg tat 384

His	Asn	Lys	Pro	Ser	Asp	Cys	Trp	Ile	Val	Val	Lys	Asn	Lys	Val	Tyr	
	115						120					125				
gat gtt tcc aat ttt gcg gac gag cat ccc gga gga tca gtt att agt 432																
Asp	Val	Ser	Asn	Phe	Ala	Asp	Glu	His	Pro	Gly	Gly	Ser	Val	Ile	Ser	
	130					135					140					
act tat ttt gga cga gac ggc aca gat gtt ttc tct agt ttt cat gca 480																
Thr	Tyr	Phe	Gly	Arg	Asp	Gly	Thr	Asp	Val	Phe	Ser	Ser	Phe	His	Ala	
145					150					155					160	
gct tct aca tgg aaa att ctt caa gac ttt tac att ggt gac gtg gag 528																
Ala	Ser	Thr	Trp	Lys	Ile	Leu	Gln	Asp	Phe	Tyr	Ile	Gly	Asp	Val	Glu	
				165					170				175			
agg gtg gag ccg act cca gag ctg ctg aaa gat ttc cga gaa atg aga 576																
Arg	Val	Glu	Pro	Thr	Pro	Glu	Leu	Leu	Lys	Asp	Phe	Arg	Glu	Met	Arg	
			180						185				190			
gct ctt ttc ctg agg gag caa ctt ttc aaa agt tcg aaa ttg tac tat 624																
Ala	Leu	Phe	Leu	Arg	Glu	Gln	Leu	Phe	Lys	Ser	Ser	Lys	Leu	Tyr	Tyr	
	195						200					205				
gtt atg aag ctg ctc acg aat gtt gct att ttt gct gcg agc att gca 672																
Val	Met	Lys	Leu	Leu	Thr	Asn	Val	Ala	Ile	Phe	Ala	Ala	Ser	Ile	Ala	
	210					215					220					
ata ata tgt tgg agc aag act att tca gcg gtt ttg gct tca gct tgt 720																
Ile	Ile	Cys	Trp	Ser	Lys	Thr	Ile	Ser	Ala	Val	Leu	Ala	Ser	Ala	Cys	
225					230					235				240		
atg atg gct ctg tgt ttc caa cag tgc gga tgg cta tcc cat gat ttt 768																
Met	Met	Ala	Leu	Cys	Phe	Gln	Gln	Cys	Gly	Trp	Leu	Ser	His	Asp	Phe	
				245					250					255		
ctc cac aat cag gtg ttt gag aca cgc tgg ctt aat gaa gtt gtc ggg 816																
Leu	His	Asn	Gln	Val	Phe	Glu	Thr	Arg	Trp	Leu	Asn	Glu	Val	Val	Gly	
			260					265					270			
tat gtg atc ggc aac gcc gtt ctg ggg ttt agt aca ggg tgg tgg aag 864																

Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys  
 275 280 285

gag aag cat aac ctt cat cat gct gct cca aat gaa tgc gat cag act 912  
 Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr  
 290 295 300

tac caa cca att gat gaa gat att gat act ctc ccc ctc att gcc tgg 960  
 Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp  
 305 310 315 320

agc aag gac ata ctg gcc aca gtt gag aat aag aca ttc ttg cga atc 1008  
 Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile  
 325 330 335

ctc caa tac cag cat ctg ttc ttc atg ggt ctg tta ttt ttc gcc cgt 1056  
 Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg  
 340 345 350

ggt agt tgg ctc ttt tgg agc tgg aga tat acc tct aca gca gtg ctc 1104  
 Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu  
 355 360 365

tca cct gtc gac agg ttg ttg gag aag gga act gtt ctg ttt cac tac 1152  
 Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr  
 370 375 380

ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc cct ggt tgg aag cca 1200  
 Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro  
 385 390 395 400

tta gta tgg atg gcg gtg act gag ctc atg tcc gcc atg ctg ctg ggc 1248  
 Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly  
 405 410 415

ttt gta ttt gta ctt agc cac aat ggg atg gag gtt tat aat tcg tct 1296  
 Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser  
 420 425 430

aaa gaa ttc gtg agt gca cag atc gta tcc aca cgg gat atc aaa gga 1344

Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly  
 435 440 445

aac ata ttc aac gac tgg ttc act ggt ggc ctt aac agg caa ata gag 1392  
 Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu  
 450 455 460

cat cat ctt ttc cca aca atg ccc agg cat aat tta aac aaa ata gca 1440  
 His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala  
 465 470 475 480

cct aga gtg gag gtg ttc tgt aag aaa cac ggt ctg gtg tac gaa gac 1488  
 Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp  
 485 490 495

gta tct att gct acc ggc act tgc aag gtt ttg aaa gca ttg aag gaa 1536  
 Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu  
 500 505 510

gtc gcg gag gct gcg gca gag cag cat gct acc acc agt taa 1578  
 Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser  
 515 520 525

<210> 18

<211> 525

<212> PRT

<213> Physcomitrella patens

<400> 18

Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn  
 1 5 10 15

Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe  
 20 25 30

Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln  
 35 40 45

Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala

50

55

60

Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly  
 65 70 75 80

Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg  
 85 90 95

Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val  
 100 105 110

His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr  
 115 120 125

Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser  
 130 135 140

Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala  
 145 150 155 160

Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu  
 165 170 175

Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg  
 180 185 190

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr  
 195 200 205

Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala  
 210 215 220

Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys  
 225 230 235 240

Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe  
 245 250 255

Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly  
 260 265 270

Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys  
 275 280 285

Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr  
 290 295 300

Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp  
 305 310 315 320

Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile  
 325 330 335

Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg  
 340 345 350

Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu  
 355 360 365

Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr  
 370 375 380

Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro  
 385 390 395 400

Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly  
 405 410 415

Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser  
 420 425 430

Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly  
 435 440 445

Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu  
 450 455 460

His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala  
 465 470 475 480

Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp  
 485 490 495

Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu  
 500 505 510

Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser  
 515 520 525

<210> 19

<211> 837

<212> DNA

<213> *Phytophthora infestans*

<220>

<221> CDS

<222> (1)..(837)

<223> Δ6-elongase

<400> 19

atg tcg act gag cta ctg cag agc tac tac gcg tgg gcc aac gcc acg 48  
 Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr  
 1 5 10 15

gag gcc aag ctg ctg gac tgg gtc gac cct gag ggc ggc tgg aag gtg 96  
 Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val  
 20 25 30

cat cct atg gca gac tac ccc cta gcc aac ttc tcc agc gtc tac gcc 144  
 His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala  
 35 40 45

atc tgc gtc gga tac ttg ctc ttc gta atc ttc ggc acg gcc ctg atg 192  
 Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met  
 50 55 60

aaa atg gga gtc ccc gcc atc aag acc agt cca tta cag ttt gtg tac 240  
 Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr  
 65 70 75 80



aac ccc atc caa gtc att gcc tgc tct tat atg tgc gtg gag gcc gcc	288
Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala	
85 90 95	
atc cag gcc tac cgc aac ggc tac acc gcc gcc ccg tgc aac gcc ttt	336
Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe	
100 105 110	
aag tcc gac gac ccc gtc atg ggc aac gtt ctg tac ctc ttc tat ctc	384
Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu	
115 120 125	
tcc aag atg ctc gac ctg tgc gac aca gtc ttc att atc cta gga aag	432
Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys	
130 135 140	
aag tgg aaa cag ctt tcc atc ttg cac gtg tac cac cac ctt acc gtg	480
Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val	
145 150 155 160	
ctt ttc gtc tac tat gtg acg ttc cgc gcc gct cag gac ggg gac tca	528
Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser	
165 170 175	
tat gct acc atc gtg ctc aac ggc ttc gtg cac acc atc atg tac act	576
Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr	
180 185 190	
tac tac ttc gtc agc gcc cac acg cgc aac att tgg tgg aag aag tac	624
Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr	
195 200 205	
ctc acg cgc att cag ctt atc cag ttc gtg acc atg aac gtg cag ggc	672
Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly	
210 215 220	
tac ctg acc tac tct cga cag tgc cca ggc atg cct cct aag gtg ccg	720
Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro	
225 230 235 240	

ctc atg tac ctt gtg tac gtg cag tca ctc ttc tgg ctc ttc atg aat 768  
 Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn  
                   245                  250                  255

ttc tac att cgc gcg tac gtg ttc ggc ccc aag aaa ccg gcc gtg gag 816  
 Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu  
                   260                  265                  270

gaa tcg aag aag aag ttg taa 837  
 Glu Ser Lys Lys Lys Leu  
                   275

<210> 20

<211> 278

<212> PRT

<213> Phytophthora infestans

<400> 20

Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr  
   1                  5                  10                  15

Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val  
                   20                  25                  30

His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala  
                   35                  40                  45

Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met  
                   50                  55                  60

Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr  
                   65                  70                  75                  80

Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala  
                   85                  90                  95

Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe  
                   100                  105                  110

Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu  
 115 120 125

Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys  
 130 135 140

Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val  
 145 150 155 160

Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser  
 165 170 175

Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr  
 180 185 190

Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr  
 195 200 205

Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly  
 210 215 220

Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro  
 225 230 235 240

Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn  
 245 250 255

Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu  
 260 265 270

Glu Ser Lys Lys Lys Leu  
 275

<210> 21

<211> 1410

<212> DNA

<213> Phaeodactylum tricornutum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1410)

&lt;223&gt; Δ5-desaturase

&lt;400&gt; 21

atg gct ccg gat gcg gat aag ctt cga caa cgc cag acg act gcg gta	48
Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val	
1 5 10 15	
gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt	96
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser	
20 25 30	
ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat	144
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr	
35 40 45	
gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt	192
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe	
50 55 60	
ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat	240
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His	
65 70 75 80	
acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gtg acg gat	288
Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp	
85 90 95	
ttc gtc tgc gag tac aag ttc gat acc gaa ttt gaa cgc gaa atc aaa	336
Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys	
100 105 110	
cga gaa gtc ttc aag att gtg cga cga ggc aag gat ttc ggt act ttg	384
Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu	
115 120 125	
gga tgg ttc ttc cgt gcg ttt tgc tac att gcc att ttc ttc tac ctg	432
Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu	

130	135	140	
cag tac cat tgg gtc acc acg gga acc tct tgg ctg ctg gcc gtg gcc			480
Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala			
145	150	155	160
tac gga atc tcc caa gcg atg att ggc atg aat gtc cag cac gat gcc			528
Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala			
165	170	175	
aac cac ggg gcc acc tcc aag cgt ccc tgg gtc aac gac atg cta ggc			576
Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly			
180	185	190	
ctc ggt gcg gat ttt att ggt ggt tcc aag tgg ctc tgg cag gaa caa			624
Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln			
195	200	205	
cac tgg acc cac cac gct tac acc aat cac gcc gag atg gat ccc gat			672
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp			
210	215	220	
agc ttt ggt gcc gaa cca atg ctc cta ttc aac gac tat ccc ttg gat			720
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp			
225	230	235	240
cat ccc gct cgt acc tgg cta cat cgc ttt caa gca ttc ttt tac atg			768
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met			
245	250	255	
ccc gtc ttg gct gga tac tgg ttg tcc gct gtc ttc aat cca caa att			816
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile			
260	265	270	
ctt gac ctc cag caa cgc ggc gca ctt tcc gtc ggt atc cgt ctc gac			864
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp			
275	280	285	
aac gct ttc att cac tcg cga cgc aag tat gcg gtt ttc tgg cgg gct			912
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala			

290	295	300	
gtg tac att gcg gtg aac gtg att gct ccg ttt tac aca aac tcc ggc			960
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly			
305	310	315	320
ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg			1008
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val			
	325	330	335
gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc			1056
Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe			
	340	345	350
gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa			1104
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu			
	355	360	365
cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt			1152
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly			
	370	375	380
gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa			1200
Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu			
385	390	395	400
cac cac ttg ttc cca cgc atg agc agc gct tgg tat ccc tac att gcc			1248
His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala			
	405	410	415
ccc aag gtc cgc gaa att tgc gcc aaa cac ggc gtc cac tac gcc tac			1296
Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr			
	420	425	430
tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac			1344
Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His			
	435	440	445
gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc			1392
Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro			

450

455

460

ttg acc gga cgg gcg taa

1410

Leu Thr Gly Arg Ala

465

470

&lt;210&gt; 22

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Phaeodactylum tricornutum

&lt;400&gt; 22

Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val

1

5

10

15

Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser

20

25

30

Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr

35

40

45

Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe

50

55

60

Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His

65

70

75

80

Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp

85

90

95

Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys

100

105

110

Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu

115

120

125

Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu

130

135

140

60

Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala  
 145 150 155 160

Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala  
 165 170 175

Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly  
 180 185 190

Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln  
 195 200 205

His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp  
 210 215 220

Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp  
 225 230 235 240

His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met  
 245 250 255

Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile  
 260 265 270

Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp  
 275- 280 285

Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala  
 290 295 300

Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly  
 305 310 315 320

Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val  
 325 330 335

Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe  
 340 345 350

Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu



355

360

365

Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly  
 370 375 380

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu  
 385 390 395 400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala  
 405 410 415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr  
 420 425 430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His  
 435 440 445

Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro  
 450 455 460

Leu Thr Gly Arg Ala  
 465

&lt;210&gt; 23

&lt;211&gt; 1344

&lt;212&gt; DNA

&lt;213&gt; Caenorhabditis elegans

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1344)

&lt;223&gt; Δ5-desaturase

&lt;400&gt; 23

atg gta tta cga gag caa gag cat gag cca ttc ttc att aaa att gat 48  
 Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp  
 1 5 10 15

gga aaa tgg tgt caa att gac gat gct gtc ctg aga tca cat cca ggt 96

62

Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly  
20 25 30

ggt agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc 144  
Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe  
35 40 45

cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa 192  
 His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu  
 50 55 60

ttg aaa aaa gag tgc cct aca caa gaa cca gag atc cca gat att aag 240  
Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys  
65 70 75 80

gat gac cca atc aaa gga att gat gat gtg aac atg gga act ttc aat 288  
Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn  
85 90 95

att tct gag aaa cga tct gcc caa ata aat aaa agt ttc act gat cta. 336  
Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu  
100 105 110

cgt atg cga gtt cgt gca gaa gga ctt atg gat gga tct cct ttg ttc 384  
 Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe  
 115 120 125

tac att aga aaa att ctt gaa aca atc ttc aca att ctt ttt gca ttc 432  
 Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe  
 130 135 140

tac	ctt	caa	tac	cac	aca	tat	tat	ctt	cca	tca	gct	att	cta	atg	gga	480
Tyr	Leu	Gln	Tyr	His	Thr	Tyr	Tyr	Leu	Pro	Ser	Ala	Ile	Leu	Met	Gly	
145					150					155					160	

gtt gcg tgg caa caa ttg gga tgg tta atc cat gaa ttc gca cat cat 528  
Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His  
165 170 175

rag ttg ttc aaa aac aga tac tac aat gat ttg gcc agc tat ttc gtt 576

Gln	Leu	Phe	Lys	Asn	Arg	Tyr	Tyr	Asn	Asp	Leu	Ala	Ser	Tyr	Phe	Val		
			180					185					190				
gga	aac	ttt	tta	caa	gga	ttc	tca	tct	ggt	ggt	tgg	aaa	gag	cag	cac	624	
Gly	Asn	Phe	Leu	Gln	Gly	Phe	Ser	Ser	Gly	Gly	Trp	Lys	Glu	Gln	His		
		195					200					205					
aat	gtg	cat	cac	gca	gcc	aca	aat	gtt	gtt	gga	cga	gac	gga	gat	ctt	672	
Asn	Val	His	His	Ala	Ala	Thr	Asn	Val	Val	Gly	Arg	Asp	Gly	Asp	Leu		
		210					215				220						
gat	tta	gtc	cca	ttc	tat	gct	aca	gtg	gca	gaa	cat	ctc	aac	aat	tat	720	
Asp	Leu	Val	Pro	Phe	Tyr	Ala	Thr	Val	Ala	Glu	His	Leu	Asn	Asn	Tyr		
225					230				235						240		
tct	cag	gat	tca	tgg	gtt	atg	act	cta	ttc	aga	tgg	caa	cat	gtt	cat	768	
Ser	Gln	Asp	Ser	Trp	Val	Met	Thr	Leu	Phe	Arg	Trp	Gln	His	Val	His		
			245						250				255				
tgg	aca	ttc	atg	tta	cca	ttc	ctc	cgt	ctc	tcg	tgg	ctt	ctt	cag	tca	816	
Trp	Thr	Phe	Met	Leu	Pro	Phe	Leu	Arg	Leu	Ser	Trp	Leu	Leu	Gln	Ser		
		260					265					270					
atc	att	ttt	gtt	agt	cag	atg	cca	act	cat	tat	tat	gac	tat	tac	aga	864	
Ile	Ile	Phe	Val	Ser	Gln	Met	Pro	Thr	His	Tyr	Tyr	Asp	Tyr	Tyr	Arg		
		275					280					285					
aat	act	gcg	att	tat	gaa	cag	gtt	ggt	ctc	tct	ttg	cac	tgg	gct	tgg	912	
Asn	Thr	Ala	Ile	Tyr	Glu	Gln	Val	Gly	Leu	Ser	Leu	His	Trp	Ala	Trp		
	290					295					300						
tca	ttg	ggt	caa	ttg	tat	ttc	cta	ccc	gat	tgg	tca	act	aga	ata	atg	960	
Ser	Leu	Gly	Gln	Leu	Tyr	Phe	Leu	Pro	Asp	Trp	Ser	Thr	Arg	Ile	Met		
305					310					315				320			
ttc	ttc	ctt	gtt	tct	cat	ctt	gtt	gga	ggt	ttc	ctg	ctc	tct	cat	gta	1008	
Phe	Phe	Leu	Val	Ser	His	Leu	Val	Gly	Gly	Phe	Leu	Leu	Ser	His	Val		
			325					330					335				
gtt	act	ttc	aat	cat	tat	tca	gtg	gag	aag	ttt	gca	ttg	agc	tcg	aac	1056	

Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn  
 340 345 350

atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg 1104  
 Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met  
 355 360 365

aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag 1152  
 Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln  
 370 375 380

att gag cac cat ctt ttc cca acg atg cca cga cac aac ttg aac act 1200  
 Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr  
 385 390 395 400

gtt atg cca ctt gtt aag gag ttt gca gca gca aat ggt tta cca tac 1248  
 Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr  
 405 410 415

atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc 1296  
 Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe  
 420 425 430

cga aat att gca aat gtt gct gct aaa ttg act aaa aag att gcc tag 1344  
 Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala  
 435 440 445

<210> 24

<211> 447

<212> PRT

<213> Caenorhabditis elegans

<400> 24

Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp  
 1 5 10 15

Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly  
 20 25 30

Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe  
 35 40 45

His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu  
 50 55 60

Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys  
 65 70 75 80

Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn  
 85 90 95

Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu  
 100 105 110

Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe  
 115 120 125

Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe  
 130 135 140

Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly  
 145 150 155 160

Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His  
 165 170 175

Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val  
 180 185 190

Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His  
 195 200 205

Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu  
 210 215 220

Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr  
 225 230 235 240

Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His

245

250

255

Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser  
 260 265 270

Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg  
 275 280 285

Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp  
 290 295 300

Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met  
 305 310 315 320

Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val  
 325 330 335

Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn  
 340 345 350

Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met  
 355 360 365

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln  
 370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr  
 385 390 395 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr  
 405 410 415

Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe  
 420 425 430

Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala  
 435 440 445

&lt;211&gt; 954

&lt;212&gt; DNA

<213> *Mortierella alpina*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(954)

<223>  $\Delta 6$ -elongase

&lt;400&gt; 25

atg gcc gcc gca atc ttg gac aag gtc aac ttc ggc att gat cag ccc 48  
 Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro  
     1                    5                    10                    15

ttc gga atc aag ctc gac acc tac ttt gct cag gcc tat gaa ctc gtc 96  
 Phe Gly Ile Lys Leu Asp Thr Tyr Phe Ala Gln Ala Tyr Glu Leu Val  
                     20                    25                    30

acc gga aag tcc atc gac tcc ttc gtc ttc cag gag ggc gtc acg cct 144  
 Thr Gly Lys Ser Ile Asp Ser Phe Val Phe Gln Glu Gly Val Thr Pro  
                     35                    40                    45

ctc tcg acc cag aga gag gtc gcc atg tgg act atc act tac ttc gtc 192  
 Leu Ser Thr Gln Arg Glu Val Ala Met Trp Thr Ile Thr Tyr Phe Val  
                     50                    55                    60

gtc atc ttt ggt ggt cgc cag atc atg aag agc cag gac gcc ttc aag 240  
 Val Ile Phe Gly Gly Arg Gln Ile Met Lys Ser Gln Asp Ala Phe Lys  
     65                    70                    75                    80

ctc aag ccc ctc ttc atc ctc cac aac ttc ctc ctg acg atc gcg tcc 288  
 Leu Lys Pro Leu Phe Ile Leu His Asn Phe Leu Leu Thr Ile Ala Ser  
                     85                    90                    95

gga tcg ctg ttg ctc ctg ttc atc gag aac ctg gtc ccc atc ctc gcc 336  
 Gly Ser Leu Leu Leu Leu Phe Ile Glu Asn Leu Val Pro Ile Leu Ala  
                     100                    105                    110

aga aac gga ctt ttc tac gcc atc tgc gac gac ggt gcc tgg acc cag 384  
 Arg Asn Gly Leu Phe Tyr Ala Ile Cys Asp Asp Gly Ala Trp Thr Gln

115	120	125	
cgc ctc gag ctc ctc tac tac ctc aac tac ctg gtc aag tac tgg gag			432
Arg Leu Glu Leu Leu Tyr Tyr Leu Asn Tyr Leu Val Lys Tyr Trp Glu			
130	135	140	
ttg gcc gac acc gtc ttt ttg gtc ctc aag aag aag cct ctt gag ttc			480
Leu Ala Asp Thr Val Phe Leu Val Leu Lys Lys Lys Pro Leu Glu Phe			
145	150	155	160
ctg cac tac ttc cac cac tcg atg acc atg gtt ctc tgc ttt gtc cag			528
Leu His Tyr Phe His His Ser Met Thr Met Val Leu Cys Phe Val Gln			
	165	170	175
ctt gga gga tac act tca gtg tcc tgg gtc cct att acc ctc aac ttg			576
Leu Gly Gly Tyr Thr Ser Val Ser Trp Val Pro Ile Thr Leu Asn Leu			
	180	185	190
act gtc cac gtc ttc atg tac tac tac tac atg cgc tcc gct gcc ggt			624
Thr Val His Val Phe Met Tyr Tyr Tyr Tyr Met Arg Ser Ala Ala Gly			
	195	200	205
gtt cgc atc tgg tgg aag cag tac ttg acc act ctc cag atc gtc cag			672
Val Arg Ile Trp Trp Lys Gln Tyr Leu Thr Thr Leu Gln Ile Val Gln			
	210	215	220
ttc gtt ctt gac ctc gga ttc atc tac ttc tgc gcc tac acc tac ttc			720
Phe Val Leu Asp Leu Gly Phe Ile Tyr Phe Cys Ala Tyr Thr Tyr Phe			
225	230	235	240
gcc ttc acc tac ttc ccc tgg gct ccc aac gtc ggc aag tgc gcc ggt			768
Ala Phe Thr Tyr Phe Pro Trp Ala Pro Asn Val Gly Lys Cys Ala Gly			
	245	250	255
acc gag ggt gct gct ctc ttt ggc tgc gga ctc ctc tcc agc tat ctc			816
Thr Glu Gly Ala Ala Leu Phe Gly Cys Gly Leu Leu Ser Ser Tyr Leu			
	260	265	270
ttg ctc ttt atc aac ttc tac cgc att acc tac aat gcc aag gcc aag			864
Leu Leu Phe Ile Asn Phe Tyr Arg Ile Thr Tyr Asn Ala Lys Ala Lys			



275

280

285

gca gcc aag gag cgt gga agc aac ttt acc ccc aag act gtc aag tcc 912  
 Ala Ala Lys Glu Arg Gly Ser Asn Phe Thr Pro Lys Thr Val Lys Ser  
 290 295 300

ggc gga tcg ccc aag aag ccc tcc aag agc aag cac atc taa 954  
 Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile  
 305 310 315

&lt;210&gt; 26

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Mortierella alpina

&lt;400&gt; 26

Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro  
 1 5 10 15

Phe Gly Ile Lys Leu Asp Thr Tyr Phe Ala Gln Ala Tyr Glu Leu Val  
 20 25 30

Thr Gly Lys Ser Ile Asp Ser Phe Val Phe Gln Glu Gly Val Thr Pro  
 35 40 45

Leu Ser Thr Gln Arg Glu Val Ala Met Trp Thr Ile Thr Tyr Phe Val  
 50 55 60

Val Ile Phe Gly Gly Arg Gln Ile Met Lys Ser Gln Asp Ala Phe Lys  
 65 70 75 80

Leu Lys Pro Leu Phe Ile Leu His Asn Phe Leu Leu Thr Ile Ala Ser  
 85 90 95

Gly Ser Leu Leu Leu Leu Phe Ile Glu Asn Leu Val Pro Ile Leu Ala  
 100 105 110

Arg Asn Gly Leu Phe Tyr Ala Ile Cys Asp Asp Gly Ala Trp Thr Gln  
 115 120 125

Arg Leu Glu Leu Leu Tyr Tyr Leu Asn Tyr Leu Val Lys Tyr Trp Glu  
 130 135 140

Leu Ala Asp Thr Val Phe Leu Val Leu Lys Lys Lys Pro Leu Glu Phe  
 145 150 155 160

Leu His Tyr Phe His His Ser Met Thr Met Val Leu Cys Phe Val Gln  
 165 170 175

Leu Gly Gly Tyr Thr Ser Val Ser Trp Val Pro Ile Thr Leu Asn Leu  
 180 185 190

Thr Val His Val Phe Met Tyr Tyr Tyr Tyr Met Arg Ser Ala Ala Gly  
 195 200 205

Val Arg Ile Trp Trp Lys Gln Tyr Leu Thr Thr Leu Gln Ile Val Gln  
 210 215 220

Phe Val Leu Asp Leu Gly Phe Ile Tyr Phe Cys Ala Tyr Thr Tyr Phe  
 225 230 235 240

Ala Phe Thr Tyr Phe Pro Trp Ala Pro Asn Val Gly Lys Cys Ala Gly  
 245 250 255

Thr Glu Gly Ala Ala Leu Phe Gly Cys Gly Leu Leu Ser Ser Tyr Leu  
 260 265 270

Leu Leu Phe Ile Asn Phe Tyr Arg Ile Thr Tyr Asn Ala Lys Ala Lys  
 275 280 285

Ala Ala Lys Glu Arg Gly Ser Asn Phe Thr Pro Lys Thr Val Lys Ser  
 290 295 300

Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile  
 305 310 315

<210> 27

<211> 1320

&lt;212&gt; DNA

&lt;213&gt; Thraustochytrium

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1320)

&lt;223&gt; Δ5-desaturase

&lt;400&gt; 27

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atg ggc aag ggc agc gag ggc cgc agc gcg gcg cgc gag atg acg gcc      48
Met Gly Lys Gly Ser Glu Gly Arg Ser Ala Ala Arg Glu Met Thr Ala
  1             5             10             15

gag gcg aac ggc gac aag cgg aaa acg att ctg atc gag ggc gtc ctg      96
Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu
          20             25             30

tac gac gcg acg aac ttt aag cac ccg ggc ggt tcg atc atc aac ttc      144
Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe
      35             40             45

ttg acc gag ggc gag gcc ggc gtg gac gcg acg cag gcg tac cgc gag      192
Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu
      50             55             60

ttt cat cag cgg tcc ggc aag gcc gac aag tac ctc aag tcg ctg ccg      240
Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro
      65             70             75             80

aag ctg gat gcg tcc aag gtg gag tcg cgg ttc tcg gcc aaa gag cag      288
Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln
          85             90             95

gcg cgg cgc gac gcc atg acg cgc gac tac gcg gcc ttt cgc gag gag      336
Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu
      100             105             110

ctc gtc gcc gag ggg tac ttt gac ccg tcg atc ccg cac atg att tac      384
Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr
      115             120             125

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cgc gtc gtg gag atc gtg gcg ctc ttc gcg ctc tcg ttc tgg ctc atg	432
Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met	
130 135 140	
tcc aag gcc tcg ccc acc tcg ctc gtg ctg ggc gtg gtg atg aac ggc	480
Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly	
145 150 155 160	
att gcg cag ggc cgc tgc ggc tgg gtc atg cac gag atg ggc cac ggg	528
Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly	
165 170 175	
tcg ttc acg ggc gtc atc tgg ctc gac gac cgg atg tgc gag ttc ttc	576
Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe	
180 185 190	
tac ggc gtc ggc tgc ggc atg agc ggg cac tac tgg aag aac cag cac	624
Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His	
195 200 205	
agc aag cac cac gcc gcg ccc aac cgc ctc gag cac gat gtc gat ctc	672
Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val Asp Leu	
210 215 220	
aac acg ctg ccc ctg gtc gcc ttt aac gag cgc gtc gtg cgc aag gtc	720
Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val Arg Lys Val	
225 230 235 240	
aag ccg gga tcg ctg ctg gcg ctc tgg ctg cgc gtg cag gcg tac ctc	768
Lys Pro Gly Ser Leu Leu Ala Leu Trp Leu Arg Val Gln Ala Tyr Leu	
245 250 255	
ttt gcg ccc gtc tcg tgc ctg ctc atc ggc ctt ggc tgg acg ctc tac	816
Phe Ala Pro Val Ser Cys Leu Leu Ile Gly Leu Gly Trp Thr Leu Tyr	
260 265 270	
ctg cac ccg cgc tac atg ctg cgc acc aag cgg cac atg gag ttc gtc	864
Leu His Pro Arg Tyr Met Leu Arg Thr Lys Arg His Met Glu Phe Val	
275 280 285	

tgg atc ttc gcg cgc tac att ggc tgg ttc tcg ctc atg ggc gct ctc	912
Trp Ile Phe Ala Arg Tyr Ile Gly Trp Phe Ser Leu Met Gly Ala Leu	
290 295 300	
ggc tac tcg ccg ggc acc tcg gtc ggg atg tac ctg tgc tcg ttc ggc	960
Gly Tyr Ser Pro Gly Thr Ser Val Gly Met Tyr Leu Cys Ser Phe Gly	
305 310 315 320	
ctc ggc tgc att tac att ttc ctg cag ttc gcc gtc agc cac acg cac	1008
Leu Gly Cys Ile Tyr Ile Phe Leu Gln Phe Ala Val Ser His Thr His	
325 330 335	
ctg ccg gtg acc aac ccg gag gac cag ctg cac tgg ctc gag tac gcg	1056
Leu Pro Val Thr Asn Pro Glu Asp Gln Leu His Trp Leu Glu Tyr Ala	
340 345 350	
gcc gac cac acg gtg aac att agc acc aag tcc tgg ctc gtc acg tgg	1104
Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp Leu Val Thr Trp	
355 360 365	
tgg atg tcg aac ctg aac ttt cag atc gag cac cac ctc ttc ccc acg	1152
Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr	
370 375 380	
gcg ccg cag ttc cgc ttc aag gaa atc agt cct cgc gtc gag gcc ctc	1200
Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu	
385 390 395 400	
ttc aag cgc cac aac ctc ccg tac tac gac ctg ccc tac acg agc gcg	1248
Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala	
405 410 415	
gtc tcg acc acc ttt gcc aat ctt tat tcc gtc ggc cac tcg gtc ggc	1296
Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly	
420 425 430	
gcc gac acc aag aag cag gac tga	1320
Ala Asp Thr Lys Lys Gln Asp	
435 440	

&lt;210&gt; 28

&lt;211&gt; 439

&lt;212&gt; PRT

&lt;213&gt; Thraustochytrium

&lt;400&gt; 28

Met Gly Lys Gly Ser Glu Gly Arg Ser Ala Ala Arg Glu Met Thr Ala  
 1 5 10 15

Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu  
 20 25 30

Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe  
 35 40 45

Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu  
 50 55 60

Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro  
 65 70 75 80

Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln  
 85 90 95

Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu  
 100 105 110

Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr  
 115 120 125

Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met  
 130 135 140

Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly  
 145 150 155 160

Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly  
 165 170 175

Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe  
 180 185 190

Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His  
 195 200 205

Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val Asp Leu  
 210 215 220

Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val Arg Lys Val  
 225 230 235 240

Lys Pro Gly Ser Leu Leu Ala Leu Trp Leu Arg Val Gln Ala Tyr Leu  
 245 250 255

Phe Ala Pro Val Ser Cys Leu Leu Ile Gly Leu Gly Trp Thr Leu Tyr  
 260 265 270

Leu His Pro Arg Tyr Met Leu Arg Thr Lys Arg His Met Glu Phe Val  
 275 280 285

Trp Ile Phe Ala Arg Tyr Ile Gly Trp Phe Ser Leu Met Gly Ala Leu  
 290 295 300

Gly Tyr Ser Pro Gly Thr Ser Val Gly Met Tyr Leu Cys Ser Phe Gly  
 305 310 315 320

Leu Gly Cys Ile Tyr Ile Phe Leu Gln Phe Ala Val Ser His Thr His  
 325 330 335

Leu Pro Val Thr Asn Pro Glu Asp Gln Leu His Trp Leu Glu Tyr Ala  
 340 345 350

Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp Leu Val Thr Trp  
 355 360 365

Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr  
 370 375 380

76

Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu  
 385 390 395 400

Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala  
 405 410 415

Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly  
 420 425 430

Ala Asp Thr Lys Lys Gln Asp  
 435

<210> 29

<211> 957

<212> DNA

<213> Mortierella alpina

<220>

<221> CDS

<222> (1)..(957)

<223> Δ6-elongase

<400> 29

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 Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu  
 1 5 10 15

ttt atg gac ctt gcc acc gct atc ggt gtc cgg gcc gcg ccc tat gtc 96  
 Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val  
 20 25 30

gat cct ctc gag gcc gcg ctg gtg gcc cag gcc gag aag tac atc ccc 144  
 Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro  
 35 40 45

acg att gtc cat cac acg cgt ggg ttc ctg gtc gcg gtg gag tcg cct 192  
 Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro  
 50 55 60



ttg gcc cgt gag ctg ccg ttg atg aac ccg ttc cac gtg ctg ttg atc	240
Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile	
65 70 75 80	
gtg ctc gct tat ttg gtc acg gtc ttt gtg ggc atg cag atc atg aag	288
Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys	
85 90 95	
aac ttt gag cgg ttc gag gtc aag acg ttt tcg ctc ctg cac aac ttt	336
Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe	
100 105 110	
tgt ctg gtc tcg atc agc gcc tac atg tgc ggt ggg atc ctg tac gag	384
Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu	
115 120 125	
gct tat cag gcc aac tat gga ctg ttt gag aac gct gct gat cat acc	432
Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr	
130 135 140	
ttc aag ggt ctt cct atg gcc aag atg atc tgg ctc ttc tac ttc tcc	480
Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser	
145 150 155 160	
aag atc atg gag ttt gtc gac acc atg atc atg gtc ctc aag aag aac	528
Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn	
165 170 175	
aac cgc cag atc tcc ttc ttg cac gtt tac cac cac agc tcc atc ttc	576
Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe	
180 185 190	
acc atc tgg tgg ttg gtc acc ttt gtt gca ccc aac ggt gaa gcc tac	624
Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr	
195 200 205	
ttc tct gct gcg ttg aac tcg ttc atc cat gtg atc atg tac ggc tac	672
Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr	
210 215 220	

78

tac ttc ttg tcg gcc ttg ggc ttc aag cag gtg tcg ttc atc aag ttc 720  
 Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe  
 225 230 235 240

tac atc acg cgc tcg cag atg aca cag ttc tgc atg atg tcg gtc cag 768  
 Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln  
 245 250 255

tct tcc tgg gac atg tac gcc atg aag gtc ctt ggc cgc ccc gga tac 816  
 Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr  
 260 265 270

ccc ttc ttc atc acg gct ctg ctt tgg ttc tac atg tgg acc atg ctc 864  
 Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu  
 275 280 285

ggt ctc ttc tac aac ttt tac aga aag aac gcc aag ttg gcc aag cag 912  
 Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln  
 290 295 300

gcc aag gcc gac gct gcc aag gag aag gca agg aag ttg cag taa 957  
 Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln  
 305 310 315

&lt;210&gt; 30

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Mortierella alpina

&lt;400&gt; 30

Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu  
 1 5 10 15

Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val  
 20 25 30

Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro  
 35 40 45

Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro  
 50 55 60

Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile  
 65 70 75 80

Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys  
 85 90 95

Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe  
 100 105 110

Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu  
 115 120 125

Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr  
 130 135 140

Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser  
 145 150 155 160

Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn  
 165 170 175

Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe  
 180 185 190

Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr  
 195 200 205

Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr  
 210 215 220

Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe  
 225 230 235 240

Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln  
 245 250 255

Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr

260

265

270

Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu  
 275 280 285

Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln  
 290 295 300

Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln  
 305 310 315

&lt;210&gt; 31

&lt;211&gt; 1374

&lt;212&gt; DNA

<213> *Mortierella alpina*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1374)

<223>  $\Delta 6$ -desaturase

&lt;400&gt; 31

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 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu  
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aat gcc gag gct ctg aat gag ggc aag aag gat gcc gag gca ccc ttc 96  
 Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe  
 20 25 30

ttg atg atc atc gac aac aag gtg tac gat gtt cgc gag ttc gtc cct 144  
 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro  
 35 40 45

gat cat ccc ggt gga agt gtg att ctc acg cac gtt ggc aag gac ggc 192  
 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly  
 50 55 60

act gac gtc ttt gac act ttt cac ccc gag gct gct tgg gag act ctt 240

Thr	Asp	Val	Phe	Asp	Thr	Phe	His	Pro	Glu	Ala	Ala	Trp	Glu	Thr	Leu	
65					70					75					80	

  

gcc aac ttt tac gtt ggt gat att gac gag agc gac cgc gat atc aag	288
Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys	
85 90 95	

  

aat gat gac ttt gcg gcc gag gtc cgc aag ctg cgt acc ttg ttc cag	336
Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln	
100 105 110	

  

tct ctt ggt tac tac gat tct tcc aag gca tac tac gcc ttc aag gtc	384
Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val	
115 120 125	

  

tcg ttc aac ctc tgc atc tgg ggt ttg tcg acg gtc att gtg gcc aag	432
Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys	
130 135 140	

  

tgg ggc cag acc tcg acc ctc gcc aac gtg ctc tcg gct gcg ctt ttg	480
Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu	
145 150 155 160	

  

ggt ctg ttc tgg cag cag tgc gga tgg ttg gct cac gac ttt ttg cat	528
Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His	
165 170 175	

  

cac cag gtc ttc cag gac cgt ttc tgg ggt gat ctt ttc ggc gcc ttc	576
His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe	
180 185 190	

  

ttg gga ggt gtc tgc cag ggc ttc tcg tcc tcg tgg tgg aag gac aag	624
Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys	
195 200 205	

  

cac aac act cac cac gcc gcc ccc aac gtc cac ggc gag gat ccc gac	672
His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp	
210 215 220	

  

att gac acc cac cct ctg ttg acc tgg agt gag cat gcg ttg gag atg	720
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Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met  
225 230 235 240

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 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe  
 245 250 255

atg gtc ctg aac cag acc tgg ttt tac ttc ccc att ctc tcg ttt gcc 816  
Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala  
260 265 270

cgt ctc tcc tgg tgc ctc cag tcc att ctc ttt gtg ctg cct aac ggt 864  
 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly  
 275 280 285

cag gcc cac aag ccc tcg ggc gcg cgt gtg ccc atc tcg ttg gtc gag 912  
Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu  
290 295 300

cag ctg tcg ctt gcg atg cac tgg acc tgg tac ctc gcc acc atg ttc 960  
Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe  
305 310 315 320

ctg ttc atc aag gat ccc gtc aac atg ctg gtg tac ttt ttg gtg tcg 1008  
Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser  
325 330 335

cag gcg gtg tgc gga aac ttg ttg gcg atc gtg ttc tcg ctc aac cac 1056  
Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His  
340 345 350

aac ggt atg cct gtg atc tcg aag gag gag gcg gtc gat atg gat ttc 1104  
 Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe  
 355 360 365

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ttc acg aag cag atc atc acg ggt cgt gat gtc cac ccg ggt cta ttt    1152
Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe
      370                375                380

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gcc aac tgg ttc acg ggt gga ttg aac tat cag atc gag cac cac ttg 1200

Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu  
 385 390 395 400

ttc cct tcg atg cct cgc cac aac ttt tca aag atc cag cct gct gtc 1248  
 Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val  
 405 410 415

gag acc ctg tgc aaa aag tac aat gtc cga tac cac acc acc ggt atg 1296  
 Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met  
 420 425 430

atc gag gga act gca gag gtc ttt agc cgt ctg aac gag gtc tcc aag 1344  
 Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys  
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gct gcc tcc aag atg ggt aag gcg cag taa 1374  
 Ala Ala Ser Lys Met Gly Lys Ala Gln  
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<210> 32

<211> 457

<212> PRT

<213> Mortierella alpina

<400> 32

Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu  
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 20 25 30

Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro  
 35 40 45

Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly  
 50 55 60

Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu  
 65 70 75 80

Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys		
85	90	95
Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln		
100	105	110
Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val		
115	120	125
Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys		
130	135	140
Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu		
145	150	155
Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His		
165	170	175
His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe		
180	185	190
Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys		
195	200	205
His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp		
210	215	220
Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met		
225	230	235
Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe		
245	250	255
Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala		
260	265	270
Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly		
275	280	285



85

Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu  
 290 295 300

Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe  
 305 310 315 320

Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser  
 325 330 335

Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His  
 340 345 350

Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe  
 355 360 365

Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe  
 370 375 380

Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu  
 385 390 395 400

Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val  
 405 410 415

Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met  
 420 425 430

Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys  
 435 440 445

Ala Ala Ser Lys Met Gly Lys Ala Gln  
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&lt;210&gt; 33

&lt;211&gt; 3598

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

<223> Sequence constitutes a plant  
promoter-terminator expression cassette in vector  
pUC19

<400> 33

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ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180  
accatatgcy gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc 240  
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aataaacaaa taggggttcc gcgcacattt ccccgaaaag tgccacctga cgtctaagaa 3540

accattatta tcatgacatt aacctataaa aataggcgta tcacgaggcc ctttcgtc 3598

<210> 34

<211> 3590

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant  
promoter-terminator expression cassette in vector  
pUC19

<400> 34

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<210> 35

<211> 3584

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant  
promoter-terminator expression cassette in vector  
pUC19

<400> 35

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<210> 36

<211> 4507

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant  
promoter-terminator expression cassette in vector  
pUC19

&lt;400&gt; 36

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&lt;210&gt; 37

&lt;211&gt; 5410

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

<223> Sequence constitutes a plant  
promoter-terminator expression cassette in vector  
pUC19

<400> 37

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<210> 38

<211> 12093

<212> DNA

<213> Unknown

<220>

<223> Plant expression vector with a  
promoter-terminator expression cassette

<400> 38

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&lt;210&gt; 39

&lt;211&gt; 12085

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

<223> Plant expression vector with a  
promoter-terminator expression cassette

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175

180

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235

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245

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365

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380

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395

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685

690

695

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 ggtaccacac aagatttgag gtgcatgaac gtcacgtgga caaaagggtt agtaattttt 15520  
 caagacaaca atgttaccac acacaagttt tgaggtgcat gcatggatgc cctgtggaaa 15580  
 gtttaaaaat attttggaat tgatttgcat ggaagccatg tgtaaaacca tgacatccac 15640  
 ttggaggatg caataatgaa gaaaactaca aatttacatg caactagtta tgcatttagt 15700  
 ctatataatg aggattttgc aatactttca ttcatacaca ctcactaagt ttacacgat 15760  
 tataatttct tcatagccag cagatctaaa atg gct ccg gat gcg gat aag ctt 15814  
 Met Ala Pro Asp Ala Asp Lys Leu  
 820 825  
 cga caa cgc cag acg act gcg gta gcg aag cac aat gct gct acc ata 15862  
 Arg Gln Arg Gln Thr Thr Ala Val Ala Lys His Asn Ala Ala Thr Ile  
 830 835 840  
 tcg acg cag gaa cgc ctt tgc agt ctg tct tcg ctc aaa ggc gaa gaa 15910  
 Ser Thr Gln Glu Arg Leu Cys Ser Leu Ser Ser Leu Lys Gly Glu Glu  
 845 850 855  
 gtc tgc atc gac gga atc atc tat gac ctc caa tca ttc gat cat ccc 15958  
 Val Cys Ile Asp Gly Ile Ile Tyr Asp Leu Gln Ser Phe Asp His Pro  
 860 865 870  
 ggg ggt gaa acg atc aaa atg ttt ggt ggc aac gat gtc act gta cag 16006  
 Gly Gly Glu Thr Ile Lys Met Phe Gly Gly Asn Asp Val Thr Val Gln



875	880	885	
tac aag atg att cac ccg tac cat acc gag aag cat ttg gaa aag atg			16054
Tyr Lys Met Ile His Pro Tyr His Thr Glu Lys His Leu Glu Lys Met			
890	895	900	905
aag cgt gtc ggc aag gtg acg gat ttc gtc tgc gag tac aag ttc gat			16102
Lys Arg Val Gly Lys Val Thr Asp Phe Val Cys Glu Tyr Lys Phe Asp			
910	915	920	
acc gaa ttt gaa cgc gaa atc aaa cga gaa gtc ttc aag att gtg cga			16150
Thr Glu Phe Glu Arg Glu Ile Lys Arg Glu Val Phe Lys Ile Val Arg			
925	930	935	
cga ggc aag gat ttc ggt act ttg gga tgg ttc ttc cgt gcg ttt tgc			16198
Arg Gly Lys Asp Phe Gly Thr Leu Gly Trp Phe Phe Arg Ala Phe Cys			
940	945	950	
tac att gcc att ttc ttc tac ctg cag tac cat tgg gtc acc acg gga			16246
Tyr Ile Ala Ile Phe Phe Tyr Leu Gln Tyr His Trp Val Thr Thr Gly			
955	960	965	
acc tct tgg ctg ctg gcc gtg gcc tac gga atc tcc caa gcg atg att			16294
Thr Ser Trp Leu Leu Ala Val Ala Tyr Gly Ile Ser Gln Ala Met Ile			
970	975	980	985
ggc atg aat gtc cag cac gat gcc aac cac ggg gcc acc tcc aag cgt			16342
Gly Met Asn Val Gln His Asp Ala Asn His Gly Ala Thr Ser Lys Arg			
990	995	1000	
ccc tgg gtc aac gac atg cta ggc ctc ggt gcg gat ttt att ggt ggt			16390
Pro Trp Val Asn Asp Met Leu Gly Leu Gly Ala Asp Phe Ile Gly Gly			
1005	1010	1015	
tcc aag tgg ctc tgg cag gaa caa cac tgg acc cac cac gct tac acc			16438
Ser Lys Trp Leu Trp Gln Glu Gln His Trp Thr His His Ala Tyr Thr			
1020	1025	1030	
aat cac gcc gag atg gat ccc gat agc ttt ggt gcc gaa cca atg ctc			16486
Asn His Ala Glu Met Asp Pro Asp Ser Phe Gly Ala Glu Pro Met Leu			

1035	1040	1045	
cta ttc aac gac tat ccc ttg gat cat ccc gct cgt acc tgg cta cat			16534
Leu Phe Asn Asp Tyr Pro Leu Asp His Pro Ala Arg Thr Trp Leu His			
1050	1055	1060	1065
cgc ttt caa gca ttc ttt tac atg ccc gtc ttg gct gga tac tgg ttg			16582
Arg Phe Gln Ala Phe Phe Tyr Met Pro Val Leu Ala Gly Tyr Trp Leu			
1070	1075	1080	
tcc gct gtc ttc aat cca caa att ctt gac ctc cag caa cgc ggc gca			16630
Ser Ala Val Phe Asn Pro Gln Ile Leu Asp Leu Gln Gln Arg Gly Ala			
1085	1090	1095	
ctt tcc gtc ggt atc cgt ctc gac aac gct ttc att cac tcg cga cgc			16678
Leu Ser Val Gly Ile Arg Leu Asp Asn Ala Phe Ile His Ser Arg Arg			
1100	1105	1110	
aag tat gcg gtt ttc tgg cgg gct gtg tac att gcg gtg aac gtg att			16726
Lys Tyr Ala Val Phe Trp Arg Ala Val Tyr Ile Ala Val Asn Val Ile			
1115	1120	1125	
gct ccg ttt tac aca aac tcc ggc ctc gaa tgg tcc tgg cgt gtc ttt			16774
Ala Pro Phe Tyr Thr Asn Ser Gly Leu Glu Trp Ser Trp Arg Val Phe			
1130	1135	1140	1145
gga aac atc atg ctc atg ggt gtg gcg gaa tcg ctc gcg ctg gcg gtc			16822
Gly Asn Ile Met Leu Met Gly Val Ala Glu Ser Leu Ala Leu Ala Val			
1150	1155	1160	
ctg ttt tcg ttg tcg cac aat ttc gaa tcc gcg gat cgc gat ccg acc			16870
Leu Phe Ser Leu Ser His Asn Phe Glu Ser Ala Asp Arg Asp Pro Thr			
1165	1170	1175	
gcc cca ctg aaa aag acg gga gaa cca gtc gac tgg ttc aag aca cag			16918
Ala Pro Leu Lys Lys Thr Gly Glu Pro Val Asp Trp Phe Lys Thr Gln			
1180	1185	1190	
gtc gaa act tcc tgc act tac ggt gga ttc ctt tcc ggt tgc ttc acg			16966
Val Glu Thr Ser Cys Thr Tyr Gly Gly Phe Leu Ser Gly Cys Phe Thr			

1195

1200

1205

gga ggt ctc aac ttt cag gtt gaa cac cac ttg ttc cca cgc atg agc 17014  
 Gly Gly Leu Asn Phe Gln Val Glu His His Leu Phe Pro Arg Met Ser  
 1210 1215 1220 1225

agc gct tgg tat ccc tac att gcc ccc aag gtc cgc gaa att tgc gcc 17062  
 Ser Ala Trp Tyr Pro Tyr Ile Ala Pro Lys Val Arg Glu Ile Cys Ala  
 1230 1235 1240

aaa cac ggc gtc cac tac gcc tac tac ccg tgg atc cac caa aac ttt 17110  
 Lys His Gly Val His Tyr Ala Tyr Tyr Pro Trp Ile His Gln Asn Phe  
 1245 1250 1255

ctc tcc acc gtc cgc tac atg cac gcg gcc ggg acc ggt gcc aac tgg 17158  
 Leu Ser Thr Val Arg Tyr Met His Ala Ala Gly Thr Gly Ala Asn Trp  
 1260 1265 1270

cgc cag atg gcc aga gaa aat ccc ttg acc gga cgg gcg taa 17200  
 Arg Gln Met Ala Arg Glu Asn Pro Leu Thr Gly Arg Ala  
 1275 1280 1285

agatctgccg gcatcgatcc cgggccatgg cctgctttaa tgagatatgc gagacgccta 17260

tgatcgcatg atatttgctt tcaattctgt tgtgcacggt gtaaaaaacc tgagcatgtg 17320

tagctcagat ccttaccgcc ggtttcggtt cattctaata aatatatcac ccgttactat 17380

cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga cgagctcggc 17440

gcgcctctag aggatcgatg aattcagatc ggctgagtgg ctcccttcaac gttgcgggttc 17500

tgtcagttcc aaacgtaaaa cggcttgtcc cgcgtcatcg gcgggggtca taacgtgact 17560

cccttaattc tccgctcatg atcagattgt cgtttcccgc cttcagttta aactatcagt 17620

gtttgacagg atatattggc gggtaaacct aagagaaaag agcgtttatt agaataatcg 17680

gatattttaa agggcgtgaa aaggtttatc cttcgtccat ttgtatgtgc atgccaacca 17740

cagggttccc ca

17752

&lt;210&gt; 47

&lt;211&gt; 290

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;400&gt; 47

Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser  
1 5 10 15

Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp  
20 25 30

Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile  
35 40 45

Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu  
50 55 60

Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu  
65 70 75 80

Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser  
85 90 95

Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr  
100 105 110

Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile  
115 120 125

Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr  
130 135 140

Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His  
145 150 155 160

Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His

201

165

170

175

His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly  
 180 185 190

Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg  
 195 200 205

Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu  
 210 215 220

Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr  
 225 230 235 240

Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile  
 245 250 255

Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr  
 260 265 270

Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys  
 275 280 285

Thr Glu  
 290

&lt;210&gt; 48

&lt;211&gt; 525

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;400&gt; 48

Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn  
 1 5 10 15

Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe  
 20 25 30

Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln

35

40

45

Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala  
 50 55 60

Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly  
 65 70 75 80

Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg  
 85 90 95

Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val  
 100 105 110

His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr  
 115 120 125

Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser  
 130 135 140

Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala  
 145 150 155 160

Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu  
 165 170 175

Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg  
 180 185 190

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr  
 195 200 205

Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala  
 210 215 220

Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys  
 225 230 235 240

Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe  
 245 250 255

Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly  
260 265 270

Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys  
275 280 285

Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr  
290 295 300

Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp  
305 310 315 320

Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile  
325 330 335

Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg  
340 345 350

Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu  
355 360 365

Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr  
370 375 380

Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro  
385 390 395 400

Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly  
405 410 415

Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser  
420 425 430

Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly  
435 440 445

Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu  
450 455 460

## 204

His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala  
 465 470 475 480

Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp  
 485 490 495

Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu  
 500 505 510

Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser  
 515 520 525

<210> 49

<211> 469

<212> PRT

<213> Unknown

<400> 49

Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val  
 1 5 10 15

Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser  
 20 25 30

Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr  
 35 40 45

Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe  
 50 55 60

Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His  
 65 70 75 80

Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp  
 85 90 95

Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys  
 100 105 110



## 205

Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu  
115 120 125

Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu  
130 135 140

Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala  
145 150 155 160

Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala  
165 170 175

Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly  
180 185 190

Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln  
195 200 205

His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp  
210 215 220

Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp  
225 230 235 240

His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met  
245 250 255

Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile  
260 265 270

Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp  
275 280 285

Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala  
290 295 300

Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly  
305 310 315 320

Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val

325

330

335

Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe  
 340 345 350

Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu  
 355 360 365

Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly  
 370 375 380

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu  
 385 390 395 400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala  
 405 410 415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr  
 420 425 430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His  
 435 440 445

Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro  
 450 455 460

Leu Thr Gly Arg Ala  
 465

&lt;210&gt; 50

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Polylinker

&lt;400&gt; 50

gaattcggcg cgccgagctc ctcgag

<210> 51

<211> 265

<212> DNA

<213> Artificial sequence

<220>

<223> Polylinker-terminator-polylinker

<400> 51

ccaccgcggt gggcgggccgc ctgcagtcta gaaggcctcc tgctttaatg agatatgcga 60  
gacgcctatg atcgcatgat atttgctttc aattctgttg tgcacgttgt aaaaaacctg 120  
agcatgtgta gctcagatcc ttaccgccgg ttctcggttca ttctaatagaa tatatcaccc 180  
gttactatcg tatttttatg aataatattc tccgttcaat ttactgattg tccgtcgacg 240  
aattcgagct cggcgcgcca agctt 265

<210> 52

<211> 257

<212> DNA

<213> Artificial sequence

<220>

<223> Polylinker-terminator-polylinker

<400> 52

ggatccgata tcgggcccgc tagcgттаac cctgctttaa tgagatatgc gagacgccta 60  
tgatcgcatg atatttgctt tcaattctgt tgtgcacgtt gtaaaaaacc tgagcatgtg 120  
tagctcagat ccttaccgcc ggtttcggtt cattctaatag aatatatcac ccgttactat 180  
cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga cgaattcgag 240  
ctcggcgcgc caagctt 257

<210> 53

<211> 257

<212> DNA

<213> Artificial sequence

<220>

<223> Polylinker-terminator-polylinker

<400> 53

agatctgccg gcatcgatcc cgggccatgg cctgctttaa tgagatatgc gagacgccta 60

tgatcgcatg atatttgctt tcaattctgt tgtgcacggt gtaaaaaacc tgagcatgtg 120

tagctcagat ccttaccgcc ggtttcggtt cattctaata aatatatcac ccgttactat 180

cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga cgaattcgag 240

ctcggcgcgc caagctt

257